

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
12 May 2005 (12.05.2005)

PCT

(10) International Publication Number
WO 2005/043168 A2

(51) International Patent Classification⁷: **G01N 33/579**,
C12Q 1/68

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(21) International Application Number:
PCT/EP2004/012470

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(22) International Filing Date:
4 November 2004 (04.11.2004)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
03025341.3 4 November 2003 (04.11.2003) EP

(81) Designated States (*unless otherwise indicated, for every
kind of national protection available*): AE, AG, AL, AM,
AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN,
CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI,
GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE,
KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD,
MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG,
PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM,
TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM,
ZW.

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(84) Designated States (*unless otherwise indicated, for every
kind of regional protection available*): ARIPO (BW, GH,
GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM,
ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM),
European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI,
FR, GB, GR, HU, IE, IS, IT, LU, MC, NL, PL, PT, RO, SE,
SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ,
GW, ML, MR, NE, SN, TD, TG).

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Published:

— *without international search report and to be republished
upon receipt of that report*

*For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.*

WO 2005/043168 A2

(54) Title: METHOD FOR DISTINGUISHING AML-SPECIFIC FLT3 LENGTH MUTATIONS FROM TKD MUTATIONS

(57) Abstract: Disclosed is a method for distinguishing AML-specific FLT3 length mutations from TKD mutations in a sample by determining the expression level of markers, as well as a diagnostic kit and an apparatus containing the markers.

Method for distinguishing AML-specific FLT3 length mutations from TKD mutations

The present invention is directed to a method for distinguishing AML-specific FLT3 length mutations from TKD mutations by determining the expression level of selected marker genes.

5 Leukemias are classified into four different groups or types: acute myeloid (AML), acute lymphatic (ALL), chronic myeloid (CML) and chronic lymphatic leukemia (CLL). Within these groups, several subcategories can be identified further using a panel of standard techniques as described below. These different subcategories in
10 leukemias are associated with varying clinical outcome and therefore are the basis for different treatment strategies. The importance of highly specific classification may be illustrated in detail further for the AML as a very heterogeneous group of diseases. Effort is aimed at identifying biological entities and to distinguish and classify subgroups of AML which are associated with a favorable, intermediate or unfavorable prognosis, respectively. In 1976, the FAB classification was proposed
15 by the French-American-British co-operative group which was based on cytomorphology and cytochemistry in order to separate AML subgroups according to the morphological appearance of blasts in the blood and bone marrow. In addition, it was recognized that genetic abnormalities occurring in the leukemic blast had a major impact on the morphological picture and even more on the
20 prognosis. So far, the karyotype of the leukemic blasts is the most important independent prognostic factor regarding response to therapy as well as survival.

Usually, a combination of methods is necessary to obtain the most important information in leukemia diagnostics: Analysis of the morphology and
25 cytochemistry of bone marrow blasts and peripheral blood cells is necessary to establish the diagnosis. In some cases the addition of immunophenotyping is mandatory to separate very undifferentiated AML from acute lymphoblastic leukemia and CLL. Leukemia subtypes investigated can be diagnosed by cytomorphology alone, only if an expert reviews the smears. However, a genetic
30 analysis based on chromosome analysis, fluorescence in situ hybridization or RT-PCR and immunophenotyping is required in order to assign all cases into the right category. The aim of these techniques besides diagnosis is mainly to determine the

prognosis of the leukemia. A major disadvantage of these methods, however, is that viable cells are necessary as the cells for genetic analysis have to divide in vitro in order to obtain metaphases for the analysis. Another problem is the long time of 72 hours from receipt of the material in the laboratory to obtain the result.

5 Furthermore, great experience in preparation of chromosomes and even more in analyzing the karyotypes is required to obtain the correct result in at least 90% of cases. Using these techniques in combination, hematological malignancies in a first approach are separated into chronic myeloid leukemia (CML), chronic lymphatic (CLL), acute lymphoblastic (ALL), and acute myeloid leukemia (AML). Within

10 the latter three disease entities several prognostically relevant subtypes have been established. As a second approach this further sub-classification is based mainly on genetic abnormalities of the leukemic blasts and clearly is associated with different prognoses.

15 The sub-classification of leukemias becomes increasingly important to guide therapy. The development of new, specific drugs and treatment approaches requires the identification of specific subtypes that may benefit from a distinct therapeutic protocol and, thus, can improve outcome of distinct subsets of leukemia. For example, the new therapeutic drug (STI571, Imatinib) inhibits the CML specific

20 chimeric tyrosine kinase BCR-ABL generated from the genetic defect observed in CML, the BCR-ABL-rearrangement due to the translocation between chromosomes 9 and 22 (t(9;22) (q34; q11)). In patients treated with this new drug, the therapy response is dramatically higher as compared to all other drugs that had been used so far. Another example is the subtype of acute myeloid leukemia AML

25 M3 and its variant M3v both with karyotype t(15;17)(q22; q11-12). The introduction of a new drug (all-trans retinoic acid - ATRA) has improved the outcome in this subgroup of patients from about 50% to 85 % long-term survivors. As it is mandatory for these patients suffering from these specific leukemia subtypes to be identified as fast as possible so that the best therapy can be applied,

30 diagnostics today must accomplish sub-classification with maximal precision. Not only for these subtypes but also for several other leukemia subtypes different treatment approaches could improve outcome. Therefore, rapid and precise identification of distinct leukemia subtypes is the future goal for diagnostics.

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Thus, the technical problem underlying the present invention was to provide means for leukemia diagnostics which overcome at least some of the disadvantages of the prior art diagnostic methods, in particular encompassing the time-consuming and unreliable combination of different methods and which provides a rapid assay to
5 unambiguously distinguish one AML subtype from another, e.g. by genetic analysis.

According to Golub et al. (Science, 1999, 286, 531-7), gene expression profiles can be used for class prediction and discriminating AML from ALL samples. However,
10 for the analysis of acute leukemias the selection of the two different subgroups was performed using exclusively morphologic-phenotypical criteria. This was only descriptive and does not provide deeper insights into the pathogenesis or the underlying biology of the leukemia. The approach reproduces only very basic knowledge of cytomorphology and intends to differentiate classes. The data is not
15 sufficient to predict prognostically relevant cytogenetic aberrations.

Furthermore, the international application WO-A 03/039443 discloses marker genes the expression levels of which are characteristic for certain leukemia, e.g. AML subtypes and additionally discloses methods for differentiating between the
20 subtype of AML cells by determining the expression profile of the disclosed marker genes. However, WO-A 03/039443 does not provide guidance which set of distinct genes discriminate between two subtypes and, as such, can be routinely taken in order to distinguish one AML subtype from another.

25 The problem is solved by the present invention, which provides a method for distinguishing AML-specific FLT3 length mutations from TKD mutations in a sample, the method comprising determining the expression level of markers selected from the markers identifiable by their Affymetrix Identification Numbers (affy ID) as defined in Tables 1, and/or 2,

30 wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.1 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.1 having a positive fc value,

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is indicative for the presence of AML_D835 when AML_D835 is distinguished from all other subtypes,

and/or wherein

5 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.2 having a negative fc value, and/or a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.2 having a positive fc value, is indicative for the presence of AML_Double when AML_Double is distinguished from all other subtypes,

10 and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.3 having a negative fc value, and/or a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.3 having a positive fc value, 15 is indicative for the presence of AML_Status-1 when AML_Status-1 is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.4 having a negative fc value, and/or 20 a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.4 having a positive fc value, is indicative for the presence of AML_Status-2 when AML_Status-2 is distinguished from all other subtypes,

and/or wherein

25 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.5 having a negative fc value, and/or a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.5 having a positive fc value, is indicative for the presence of AML_Status-3 when AML_Status-3 is 30 distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.6 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.6 having a positive fc value,
5 is indicative for the presence of AML_Status-4 when AML_Status-4 is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.7 having a negative fc value, and/or
10 a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.7 having a positive fc value,
is indicative for the presence of AML_Status-5 when AML_Status-5 is distinguished from all other subtypes,

and/or wherein

15 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.8 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.8 having a positive fc value,
is indicative for the presence of AML_normal when AML_normal is
20 distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.1 having a negative fc value, and/or
25 a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.1 having a positive fc value,
is indicative for the presence of AML_D835 when AML_D835 is distinguished from AML_Double,

and/or wherein

30 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.2 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.2 having a positive fc value,
is indicative for the presence of AML_D835 when AML_D835 is distinguished from AML_Status-1,

5 and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.3 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.3 having a positive fc value,
10 is indicative for the presence of AML_D835 when AML_D835 is distinguished from AML_Status-2,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.4 having a negative fc value, and/or
15 a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.4 having a positive fc value,
is indicative for the presence of AML_D835 when AML_D835 is distinguished from AML_Status-3,

and/or wherein

20 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.5 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.5 having a positive fc value,
is indicative for the presence of AML_D835 when AML_D835 is distinguished from AML_Status-4,
25

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.6 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.6 having a positive fc value,
30

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is indicative for the presence of AML_D835 when AML_D835 is distinguished from AML_Status-5,

and/or wherein

5 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.7 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.7 having a positive fc value,
is indicative for the presence of AML_D835 when AML_D835 is distinguished from AML_normal,

10 and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.8 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.8 having a positive fc value,
15 is indicative for the presence of AML_Double when AML_Double is distinguished from AML_Status-1,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.9 having a negative fc value, and/or
20 a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.9 having a positive fc value,
is indicative for the presence of AML_Double when AML_Double is distinguished from AML_Status-2,

and/or wherein

25 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.10 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.10 having a positive fc value,
is indicative for the presence of AML_Double when AML_Double is distinguished from AML_Status-3,
30

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.11 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.11 having a positive fc value,
5 is indicative for the presence of AML_Double when AML_Double is distinguished from AML_Status-4,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.12 having a negative fc value, and/or
10 a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.12 having a positive fc value,
is indicative for the presence of AML_Double when AML_Double is distinguished from AML_Status-5,

and/or wherein

15 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.13 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.13 having a positive fc value,
is indicative for the presence of AML_Double when AML_Double is
20 distinguished from AML_normal,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.14 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least
25 one of the numbers 1 to 50 of Table 2.14 having a positive fc value,
is indicative for the presence of AML_Status-1 when AML_Status-1 is distinguished from AML_Status-2,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one
30 of the numbers 1 to 50 of Table 2.15 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.15 having a positive fc value,
is indicative for the presence of AML_Status-1 when AML_Status-1 is distinguished from AML_Status-3,

5 and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.16 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.16 having a positive fc value,
10 is indicative for the presence of AML_Status-1 when AML_Status-1 is distinguished from AML_Status-4,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.17 having a negative fc value, and/or
15 a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.17 having a positive fc value,
is indicative for the presence of AML_Status-1 when AML_Status-1 is distinguished from AML_Status-5,

and/or wherein

20 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.18 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.18 having a positive fc value,
is indicative for the presence of AML_Status-1 when AML_Status-1 is
25 distinguished from AML_normal,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.19 having a negative fc value, and/or
30 a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.19 having a positive fc value,

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is indicative for the presence of AML_Status-2 when AML_Status-2 is distinguished from AML_Status-3,

and/or wherein

5 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.20 having a negative fc value, and/or a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.20 having a positive fc value, is indicative for the presence of AML_Status-2 when AML_Status-2 is distinguished from AML_Status-4,

10 and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.21 having a negative fc value, and/or a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.21 having a positive fc value, 15 is indicative for the presence of AML_Status-2 when AML_Status-2 is distinguished from AML_Status-5,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.22 having a negative fc value, and/or 20 a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.22 having a positive fc value, is indicative for the presence of AML_Status-2 when AML_Status-2 is distinguished from AML_normal,

and/or wherein

25 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.23 having a negative fc value, and/or a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.23 having a positive fc value, is indicative for the presence of AML_Status-3 when AML_Status-3 is 30 distinguished from AML_Status-4,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.24 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.24 having a positive fc value,
5 is indicative for the presence of AML_Status-3 when AML_Status-3 is distinguished from AML_Status-5,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.25 having a negative fc value, and/or
10 a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.25 having a positive fc value,
is indicative for the presence of AML_Status-3 when AML_Status-3 is distinguished from AML_normal,

and/or wherein

15 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.26 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.26 having a positive fc value,
is indicative for the presence of AML_Status-4 when AML_Status-4 is distinguished from AML_Status-5,
20

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.27 having a negative fc value, and/or
25 a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.27 having a positive fc value,
is indicative for the presence of AML_Status-4 when AML_Status-4 is distinguished from AML_normal,

and/or wherein

30 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.28 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.28 having a positive fc value, is indicative for the presence of AML_Status-5 when AML_Status-5 is distinguished from AML_normal.

5

FLT3 stands for FMS-like tyrosine kinase 3. TKD stand for tyrosin kinase domain of FLT3.

10

Two mayor types of mutations in the FLT3-Gene have been described.

- 1) Length mutations in the juxtamembrane domain (FLT3-LM, status 1, 2, 3, 4, 5)
- 2) point mutations in codons D835 or I836 or deletions of I836 in the tyrosine kinase domain (all coded as D835, refers to TKD mutation).
- 3) "Double" means that both types of mutations were found in a single patient.

15

As used herein, the abbreviations used above apply for the following AML subtypes (see Also Example 1):

- 1) AML_normal (normal karyotype) and no FLT3 mutation,
- 2) AML_status 1: FLT3-LM/WT (wildtype) ratio <0.3,
- 20 3) AML_status 2: ratio 0.7-1.1 ,
- 4) AML_status 3: ratio of >1.2=partial loss of WT (wild type),
- 5) AML_status 4: total loss of WT ,
- 6) AML_status 5: two or more low status mutations
- 7) AML_D835: D835/TKD mutation (mutation in the tyrosine kinase domain of FLT3)
- 25 8) AML_Double: mutations D835/TKD and FLT3-LM

30

As used herein, "all other subtypes" refer to the subtypes of the present invention, i.e. if one subtype is distinguished from "all other subtypes", it is distigished from all other subtypes contained in the present invention.

According to the present invention, a "sample" means any biological material containing genetic information in the form of nucleic acids or proteins obtainable or obtained from an individual. The sample includes e.g. tissue samples, cell

5 samples, bone marrow and/or body fluids such as blood, saliva, semen. Preferably, the sample is blood or bone marrow, more preferably the sample is bone marrow. The person skilled in the art is aware of methods, how to isolate nucleic acids and proteins from a sample. A general method for isolating and preparing nucleic acids from a sample is outlined in Example 3.

10 According to the present invention, the term "lower expression" is generally assigned to all by numbers and Affymetrix ID. definable polynucleotides the t-values and fold change (fc) values of which are negative, as indicated in the Tables. Accordingly, the term "higher expression" is generally assigned to all by numbers and Affymetrix ID. definable polynucleotides the t-values and fold change (fc) values of which are positive.

15 According to the present invention, the term "expression" refers to the process by which mRNA or a polypeptide is produced based on the nucleic acid sequence of a gene, i.e. „expression“ also includes the formation of mRNA upon transcription. In accordance with the present invention, the term „determining the expression level“ preferably refers to the determination of the level of expression, namely of the markers.

20 Generally, "marker" refers to any genetically controlled difference which can be used in the genetic analysis of a test versus a control sample, for the purpose of assigning the sample to a defined genotype or phenotype. As used herein, "markers" refer to genes which are differentially expressed in, e.g., different AML
25 subtypes. The markers can be defined by their gene symbol name, their encoded protein name, their transcript identification number (cluster identification number), the data base accession number, public accession number or GenBank identifier or, as done in the present invention, Affymetrix identification number, chromosomal location, UniGene accession number and cluster type, LocusLink accession number
30 (see Examples and Tables).

The Affymetrix identification number (affy ID) is accessible for anyone and the person skilled in the art by entering the "gene expression omnibus" internet page of the National Center for Biotechnology Information (NCBI)

(<http://www.ncbi.nlm.nih.gov/geo/>). In particular, the affy ID's of the polynucleotides used for the method of the present invention are derived from the so-called U133 chip. The sequence data of each identification number can be viewed at <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL96>

5

Generally, the expression level of a marker is determined by the determining the expression of its corresponding "polynucleotide" as described hereinafter.

10 According to the present invention, the term „polynucleotide“ refers, generally, to a DNA, in particular cDNA, or RNA, in particular a cRNA, or a portion thereof or a polypeptide or a portion thereof. In the case of RNA (or cDNA), the polynucleotide is formed upon transcription of a nucleotide sequence which is capable of expression. The polynucleotide fragments refer to fragments preferably of between at least 8, such as 10, 12, 15 or 18 nucleotides and at least 50, such as 60, 80, 100,
15 200 or 300 nucleotides in length, or a complementary sequence thereto, representing a consecutive stretch of nucleotides of a gene, cDNA or mRNA. In other terms, polynucleotides include also any fragment (or complementary sequence thereto) of a sequence derived from any of the markers defined above as long as these fragments unambiguously identify the marker.

20

The determination of the expression level may be effected at the transcriptional or translational level, i.e. at the level of mRNA or at the protein level. Protein fragments such as peptides or polypeptides advantageously comprise between at least 6 and at least 25, such as 30, 40, 80, 100 or 200 consecutive amino acids
25 representative of the corresponding full length protein. Six amino acids are generally recognized as the lowest peptidic stretch giving rise to a linear epitope recognized by an antibody, fragment or derivative thereof. Alternatively, the proteins or fragments thereof may be analysed using nucleic acid molecules specifically binding to three-dimensional structures (aptamers).

30

Depending on the nature of the polynucleotide or polypeptide, the determination of the expression levels may be effected by a variety of methods. For determining and detecting the expression level, it is preferred in the present invention that the polynucleotide, in particular the cRNA, is labelled.

The labelling of the polynucleotide or a polypeptide can occur by a variety of methods known to the skilled artisan. The label can be fluorescent, chemiluminescent, bioluminescent, radioactive (such as ^3H or ^{32}P). The labelling compound can be any labelling compound being suitable for the labelling of polynucleotides and/or polypeptides. Examples include fluorescent dyes, such as fluorescein, dichlorofluorescein, hexachlorofluorescein, BODIPY variants, ROX, tetramethylrhodamin, rhodamin X, Cyanine-2, Cyanine-3, Cyanine-5, Cyanine-7, IRD40, FluorX, Oregon Green, Alexa variants (available e.g. from Molecular Probes or Amersham Biosciences) and the like, biotin or biotinylated nucleotides, digoxigenin, radioisotopes, antibodies, enzymes and receptors. Depending on the type of labelling, the detection is done via fluorescence measurements, conjugation to streptavidin and/or avidin, antigen-antibody- and/or antibody-antibody-interactions, radioactivity measurements, as well as catalytic and/or receptor/ligand interactions. Suitable methods include the direct labelling (incorporation) method, the amino-modified (amino-allyl) nucleotide method (available e.g. from Ambion), and the primer tagging method (DNA dendrimer labelling, as kit available e.g. from Genisphere). Particularly preferred for the present invention is the use of biotin or biotinylated nucleotides for labelling, with the latter being directly incorporated into, e.g. the cRNA polynucleotide by in vitro transcription.

If the polynucleotide is mRNA, cDNA may be prepared into which a detectable label, as exemplified above, is incorporated. Said detectably labelled cDNA, in single-stranded form, may then be hybridised, preferably under stringent or highly stringent conditions to a panel of single-stranded oligonucleotides representing different genes and affixed to a solid support such as a chip. Upon applying appropriate washing steps, those cDNAs will be detected or quantitatively detected that have a counterpart in the oligonucleotide panel. Various advantageous embodiments of this general method are feasible. For example, the mRNA or the cDNA may be amplified e.g. by polymerase chain reaction, wherein it is preferable, for quantitative assessments, that the number of amplified copies corresponds relative to further amplified mRNAs or cDNAs to the number of mRNAs originally present in the cell. In a preferred embodiment of the present invention, the cDNAs are transcribed into cRNAs prior to the hybridisation step wherein only in the transcription step a label is incorporated into the nucleic acid

and wherein the cRNA is employed for hybridisation. Alternatively, the label may be attached subsequent to the transcription step.

Similarly, proteins from a cell or tissue under investigation may be contacted with a panel of aptamers or of antibodies or fragments or derivatives thereof. The antibodies etc. may be affixed to a solid support such as a chip. Binding of proteins indicative of an AML subtype may be verified by binding to a detectably labelled secondary antibody or aptamer. For the labelling of antibodies, it is referred to Harlow and Lane, "Antibodies, a laboratory manual", CSH Press, 1988, Cold Spring Harbor. Specifically, a minimum set of proteins necessary for diagnosis of all AML subtypes may be selected for creation of a protein array system to make diagnosis on a protein lysate of a diagnostic bone marrow sample directly. Protein Array Systems for the detection of specific protein expression profiles already are available (for example: Bio-Plex, BIORAD, München, Germany). For this application preferably antibodies against the proteins have to be produced and immobilized on a platform e.g. glassslides or microtiterplates. The immobilized antibodies can be labelled with a reactant specific for the certain target proteins as discussed above. The reactants can include enzyme substrates, DNA, receptors, antigens or antibodies to create for example a capture sandwich immunoassay.

For reliably distinguishing AML-specific FLT3 length mutations from TKD mutations it is useful that the expression of more than one of the above defined markers is determined. As a criterion for the choice of markers, the statistical significance of markers as expressed in q or p values based on the concept of the false discovery rate is determined. In doing so, a measure of statistical significance called the q value is associated with each tested feature. The q value is similar to the p value, except it is a measure of significance in terms of the false discovery rate rather than the false positive rate (Storey JD and Tibshirani R. Proc.Natl.Acad.Sci., 2003, Vol. 100:9440-5).

In a preferred embodiment of the present invention, markers as defined in Tables 1-2 having a q -value of less than, $3E-02$, less than $3E-06$, more preferred less than $1.5E-09$, most preferred less than $1.5E-11$, less than $1.5E-20$, less than $1.5E-30$, are measured.

Of the above defined markers, the expression level of at least two, preferably of at least ten, more preferably of at least 25, most preferably of 50 of at least one of the Tables of the markers is determined.

- 5 In another preferred embodiment, the expression level of at least 2, of at least 5, of at least 10 out of the markers having the numbers 1 – 10, 1-20, 1-40, 1-50 of at least one of the Tables are measured.

- 10 The level of the expression of the „marker“, i.e. the expression of the polynucleotide is indicative of the AML subtype of a cell or an organism. The level of expression of a marker or group of markers is measured and is compared with the level of expression of the same marker or the same group of markers from other cells or samples. The comparison may be effected in an actual experiment or in silico. When the expression level also referred to as expression pattern or
15 expression signature (expression profile) is measurably different, there is according to the invention a meaningful difference in the level of expression. Preferably the difference at least is 5 %, 10% or 20%, more preferred at least 50% or may even be as high as 75% or 100%. More preferred the difference in the level of expression is at least 200%, i.e. two fold, at least 500%, i.e. five fold, or at least 1000%, i.e. 10
20 fold.

- Accordingly, the expression level of markers expressed lower in a first subtype than in at least one second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e.
25 2-fold lower, preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold lower in the first subtype. On the other hand, the expression level of markers expressed higher in a first subtype than in at least one second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold higher,
30 preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold higher in the first subtype.

- In another embodiment of the present invention, the sample is derived from an individual having leukemia, preferably AML.

- For the method of the present invention it is preferred if the polynucleotide the expression level of which is determined is in form of a transcribed polynucleotide. A particularly preferred transcribed polynucleotide is an mRNA, a cDNA and/or a cRNA, with the latter being preferred. Transcribed polynucleotides are isolated from a sample, reverse transcribed and/or amplified, and labelled, by employing methods well-known the person skilled in the art (see Example 3). In a preferred embodiment of the methods according to the invention, the step of determining the expression profile further comprises amplifying the transcribed polynucleotide.
- 10 In order to determine the expression level of the transcribed polynucleotide by the method of the present invention, it is preferred that the method comprises hybridizing the transcribed polynucleotide to a complementary polynucleotide, or a portion thereof, under stringent hybridization conditions, as described hereinafter.
- 15 The term "hybridizing" means hybridization under conventional hybridization conditions, preferably under stringent conditions as described, for example, in Sambrook, J., et al., in "Molecular Cloning: A Laboratory Manual" (1989), Eds. J. Sambrook, E. F. Fritsch and T. Maniatis, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, NY and the further definitions provided above. Such conditions are, for example, hybridization in 6x SSC, pH 7.0 / 0.1% SDS at about 45°C for 18-23 hours, followed by a washing step with 2x SSC/0.1% SDS at 50°C. In order to select the stringency, the salt concentration in the washing step can for example be chosen between 2x SSC/0.1% SDS at room temperature for low stringency and 0.2x SSC/0.1% SDS at 50°C for high stringency. In addition, the temperature of the washing step can be varied between room temperature, ca. 22°C, for low stringency, and 65°C to 70° C for high stringency. Also contemplated are polynucleotides that hybridize at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation, preferably of formamide concentration (lower percentages of formamide result in lowered stringency), salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 mg/ml salmon sperm blocking DNA, followed by washes at 50°C with 1 X SSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5x SSC). Variations in the above conditions may be accomplished through the inclusion

and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

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“Complementary” and “complementarity”, respectively, can be described by the percentage, i.e. proportion, of nucleotides which can form base pairs between two polynucleotide strands or within a specific region or domain of the two strands. Generally, complementary nucleotides are, according to the base pairing rules, adenine and thymine (or adenine and uracil), and cytosine and guanine. Complementarity may be partial, in which only some of the nucleic acids' bases are matched according to the base pairing rules. Or, there may be a complete or total complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has effects on the efficiency and strength of hybridization between nucleic acid strands.

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Two nucleic acid strands are considered to be 100% complementary to each other over a defined length if in a defined region all adenines of a first strand can pair with a thymine (or an uracil) of a second strand, all guanines of a first strand can pair with a cytosine of a second strand, all thymine (or uracils) of a first strand can pair with an adenine of a second strand, and all cytosines of a first strand can pair with a guanine of a second strand, and vice versa. According to the present invention, the degree of complementarity is determined over a stretch of 20, preferably 25, nucleotides, i.e. a 60% complementarity means that within a region of 20 nucleotides of two nucleic acid strands 12 nucleotides of the first strand can base pair with 12 nucleotides of the second strand according to the above ruling, either as a stretch of 12 contiguous nucleotides or interspersed by non-pairing nucleotides, when the two strands are attached to each other over said region of 20 nucleotides. The degree of complementarity can range from at least about 50% to full, i.e. 100% complementarity. Two single nucleic acid strands are said to be “substantially complementary” when they are at least about 80% complementary, preferably about 90% or higher. For carrying out the method of the present invention substantial complementarity is preferred.

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Preferred methods for detection and quantification of the amount of polynucleotides, i.e. for the methods according to the invention allowing the determination of the level of expression of a marker, are those described by

- 20 -

5 Sambrook et al. (1989) or real time methods known in the art as the TaqMan® method disclosed in WO92/02638 and the corresponding U.S. 5,210,015, U.S. 5,804,375, U.S. 5,487,972. This method exploits the exonuclease activity of a polymerase to generate a signal. In detail, the (at least one) target nucleic acid component is detected by a process comprising contacting the sample with an oligonucleotide containing a sequence complementary to a region of the target nucleic acid component and a labeled oligonucleotide containing a sequence complementary to a second region of the same target nucleic acid component sequence strand, but not including the nucleic acid sequence defined by the first oligonucleotide, to create a mixture of duplexes during hybridization conditions, wherein the duplexes comprise the target nucleic acid annealed to the first oligonucleotide and to the labeled oligonucleotide such that the 3'-end of the first oligonucleotide is adjacent to the 5'-end of the labeled oligonucleotide. Then this mixture is treated with a template-dependent nucleic acid polymerase having a 5' to 3' nuclease activity under conditions sufficient to permit the 5' to 3' nuclease activity of the polymerase to cleave the annealed, labeled oligonucleotide and release labeled fragments. The signal generated by the hydrolysis of the labeled oligonucleotide is detected and/ or measured. TaqMan® technology eliminates the need for a solid phase bound reaction complex to be formed and made detectable. Other methods include e.g. fluorescence resonance energy transfer between two adjacently hybridized probes as used in the LightCycler® format described in U.S. 6,174,670.

25 A preferred protocol if the marker, i.e. the polynucleotide, is in form of a transcribed nucleotide, is described in Example 3, where total RNA is isolated, cDNA and, subsequently, cRNA is synthesized and biotin is incorporated during the transcription reaction. The purified cRNA is applied to commercially available arrays which can be obtained e.g. from Affymetrix. The hybridized cRNA is detected according to the methods described in Example 3. The arrays are produced by photolithography or other methods known to experts skilled in the art e.g. from U.S. 5,445,934, U.S. 5,744,305, U.S. 5,700,637, U.S. 5,945,334 and EP 0 619 321 or EP 0 373 203, or as described hereinafter in greater detail.

35 In another embodiment of the present invention, the polynucleotide or at least one of the polynucleotides is in form of a polypeptide. In another preferred embodiment, the expression level of the polynucleotides or polypeptides is detected

using a compound which specifically binds to the polynucleotide of the polypeptide of the present invention.

5 As used herein, "specifically binding" means that the compound is capable of discriminating between two or more polynucleotides or polypeptides, i.e. it binds to the desired polynucleotide or polypeptide, but essentially does not bind unspecifically to a different polynucleotide or polypeptide.

10 The compound can be an antibody, or a fragment thereof, an enzyme, a so-called small molecule compound, a protein-scaffold, preferably an anticalin. In a preferred embodiment, the compound specifically binding to the polynucleotide or polypeptide is an antibody, or a fragment thereof.

15 As used herein, an "antibody" comprises monoclonal antibodies as first described by Köhler and Milstein in Nature 278 (1975), 495-497 as well as polyclonal antibodies, i.e. antibodies contained in a polyclonal antiserum. Monoclonal antibodies include those produced by transgenic mice. Fragments of antibodies include F(ab')₂, Fab and Fv fragments. Derivatives of antibodies include scFvs, chimeric and humanized antibodies. See, for example Harlow and Lane, loc. cit.
20 For the detection of polypeptides using antibodies or fragments thereof, the person skilled in the art is aware of a variety of methods, all of which are included in the present invention. Examples include immunoprecipitation, Western blotting, Enzyme-linked immuno sorbent assay (ELISA), Enzyme-linked immuno sorbent assay (RIA), dissociation-enhanced lanthanide fluoro immuno assay (DELFI),
25 scintillation proximity assay (SPA). For detection, it is desirable if the antibody is labelled by one of the labelling compounds and methods described supra.

30 In another preferred embodiment of the present invention, the method for distinguishing AML-specific FLT3 length mutations from TKD mutations is carried out on an array.

35 In general, an "array" or "microarray" refers to a linear or two- or three dimensional arrangement of preferably discrete nucleic acid or polypeptide probes which comprises an intentionally created collection of nucleic acid or polypeptide probes of any length spotted onto a substrate/solid support. The person skilled in

the art knows a collection of nucleic acids or polypeptide spotted onto a substrate/solid support also under the term "array". As known to the person skilled in the art, a microarray usually refers to a miniaturised array arrangement, with the probes being attached to a density of at least about 10, 20, 50, 100 nucleic acid molecules referring to different or the same genes per cm². Furthermore, where appropriate an array can be referred to as "gene chip". The array itself can have different formats, e.g. libraries of soluble probes or libraries of probes tethered to resin beads, silica chips, or other solid supports.

The process of array fabrication is well-known to the person skilled in the art. In the following, the process for preparing a nucleic acid array is described. Commonly, the process comprises preparing a glass (or other) slide (e.g. chemical treatment of the glass to enhance binding of the nucleic acid probes to the glass surface), obtaining DNA sequences representing genes of a genome of interest, and spotting sequences these sequences of interest onto glass slide. Sequences of interest can be obtained via creating a cDNA library from an mRNA source or by using publicly available databases, such as GeneBank, to annotate the sequence information of custom cDNA libraries or to identify cDNA clones from previously prepared libraries. Generally, it is recommendable to amplify obtained sequences by PCR in order to have sufficient amounts of DNA to print on the array. The liquid containing the amplified probes can be deposited on the array by using a set of microspotting pins. Ideally, the amount deposited should be uniform. The process can further include UV-crosslinking in order to enhance immobilization of the probes on the array.

In a preferred embodiment, the array is a high density oligonucleotide (oligo) array using a light-directed chemical synthesis process, employing the so-called photolithography technology. Unlike common cDNA arrays, oligo arrays (according to the Affymetrix technology) use a single-dye technology. Given the sequence information of the markers, the sequence can be synthesized directly onto the array, thus, bypassing the need for physical intermediates, such as PCR products, required for making cDNA arrays. For this purpose, the marker, or partial sequences thereof, can be represented by 14 to 20 features, preferably by less than 14 features, more preferably less than 10 features, even more preferably by 6 features or less, with each feature being a short sequence of nucleotides (oligonucleotide), which is a perfect match (PM) to a segment of the respective gene. The PM oligonucleotide are paired with mismatch (MM) oligonucleotides

which have a single mismatch at the central base of the nucleotide and are used as "controls". The chip exposure sites are defined by masks and are deprotected by the use of light, followed by a chemical coupling step resulting in the synthesis of one nucleotide. The masking, light deprotection, and coupling process can then be repeated to synthesize the next nucleotide, until the nucleotide chain is of the specified length.

Advantageously, the method of the present invention is carried out in a robotics system including robotic plating and a robotic liquid transfer system, e.g. using microfluidics, i.e. channelled structured.

A particular preferred method according to the present invention is as follows:

1. Obtaining a sample, e.g. bone marrow or peripheral blood aliquots, from a patient having AML
2. Extracting RNA, preferably mRNA, from the sample
3. Reverse transcribing the RNA into cDNA
4. In vitro transcribing the cDNA into cRNA
5. Fragmenting the cRNA
6. Hybridizing the fragmented cRNA on standard microarrays
7. Determining hybridization

In another embodiment, the present invention is directed to the use of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy ID) as defined in Tables 1, and/or 2 for the manufacturing of a diagnostic for distinguishing AML-specific FLT3 length mutations from TKD mutations. The use of the present invention is particularly advantageous for distinguishing AML-specific FLT3 length mutations from TKD mutations in an individual having AML. The use of said markers for diagnosis of AML-specific FLT3 length mutations from TKD mutations, preferably based on microarray technology, offers the following advantages: (1) more rapid and more precise diagnosis, (2) easy to use in laboratories without specialized experience, (3) abolishes the requirement for analyzing viable cells for chromosome analysis (transport problem), and (4) very experienced hematologists for cytomorphology and cytochemistry, immunophenotyping as well as cytogeneticists and molecularbiologists are no longer required.

Accordingly, the present invention refers to a diagnostic kit containing at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy ID) as defined in Tables 1, and/or 2 for distinguishing AML-specific FLT3 length mutations from TKD mutations, in combination with suitable auxiliaries. Suitable auxiliaries, as used herein, include buffers, enzymes, labelling compounds, and the like. In a preferred embodiment, the marker contained in the kit is a nucleic acid molecule which is capable of hybridizing to the mRNA corresponding to at least one marker of the present invention. Preferably, the at least one nucleic acid molecule is attached to a solid support, e.g. a polystyrene microtiter dish, nitrocellulose membrane, glass surface or to non-immobilized particles in solution.

In another preferred embodiment, the diagnostic kit contains at least one reference for an AML-specific FLT3 length mutation and/or TKD mutation. As used herein, the reference can be a sample or a data bank.

In another embodiment, the present invention is directed to an apparatus for distinguishing AML-specific FLT3 length mutations from TKD mutations in a sample, containing a reference data bank obtainable by comprising

- (a) compiling a gene expression profile of a patient sample by determining the expression level at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy ID) as defined in Tables 1, and/or 2, and
- (b) classifying the gene expression profile by means of a machine learning algorithm.

According to the present invention, the "machine learning algorithm" is a computational-based prediction methodology, also known to the person skilled in the art as "classifier", employed for characterizing a gene expression profile. The signals corresponding to a certain expression level which are obtained by the microarray hybridization are subjected to the algorithm in order to classify the expression profile. Supervised learning involves "training" a classifier to recognize the distinctions among classes and then "testing" the accuracy of the classifier on an independent test set. For new, unknown samples the classifier shall predict into which class the sample belongs.

Preferably, the machine learning algorithm is selected from the group consisting of Weighted Voting, K-Nearest Neighbors, Decision Tree Induction, Support Vector Machines (SVM), and Feed-Forward Neural Networks. Most preferably, the machine learning algorithm is Support Vector Machine, such as polynomial kernel and Gaussian Radial Basis Function-kernel SVM models.

The classification accuracy of a given gene list for a set of microarray experiments is preferably estimated using Support Vector Machines (SVM), because there is evidence that SVM-based prediction slightly outperforms other classification techniques like k-Nearest Neighbors (k-NN). The LIBSVM software package version 2.36 was used (SVM-type: C-SVC, linear kernel (<http://www.csie.ntu.edu.tw/~cjlin/libsvm/>)). The skilled artisan is furthermore referred to Brown et al., Proc.Natl.Acad.Sci., 2000; 97: 262-267, Furey et al., Bioinformatics. 2000; 16: 906-914, and Vapnik V. Statistical Learning Theory. New York: Wiley, 1998.

In detail, the classification accuracy of a given gene list for a set of microarray experiments can be estimated using Support Vector Machines (SVM) as supervised learning technique. Generally, SVMs are trained using differentially expressed genes which were identified on a subset of the data and then this trained model is employed to assign new samples to those trained groups from a second and different data set. Differentially expressed genes were identified applying ANOVA and t-test-statistics (Welch t-test). Based on identified distinct gene expression signatures respective training sets consisting of 2/3 of cases and test sets with 1/3 of cases to assess classification accuracies are designated. Assignment of cases to training and test set is randomized and balanced by diagnosis. Based on the training set a Support Vector Machine (SVM) model is built.

According to the present invention, the apparent accuracy, i.e. the overall rate of correct predictions of the complete data set was estimated by 10fold cross validation. This means that the data set was divided into 10 approximately equally sized subsets, an SVM-model was trained for 9 subsets and predictions were generated for the remaining subset. This training and prediction process was repeated 10 times to include predictions for each subset. Subsequently the data set was split into a training set, consisting of two thirds of the samples, and a test set

with the remaining one third. Apparent accuracy for the training set was estimated by 10fold cross validation (analogous to apparent accuracy for complete set). A SVM-model of the training set was built to predict diagnosis in the independent test set, thereby estimating true accuracy of the prediction model. This prediction approach was applied both for overall classification (multi-class) and binary classification (diagnosis $X \Rightarrow$ yes or no). For the latter, sensitivity and specificity were calculated:

Sensitivity = (number of positive samples predicted)/(number of true positives)

Specificity = (number of negative samples predicted)/(number of true negatives)

In a preferred embodiment, the reference data bank is backed up on a computational data memory chip which can be inserted in as well as removed from the apparatus of the present invention, e.g. like an interchangeable module, in order to use another data memory chip containing a different reference data bank.

The apparatus of the present invention containing a desired reference data bank can be used in a way such that an unknown sample is, first, subjected to gene expression profiling, e.g. by microarray analysis in a manner as described supra or in the art, and the expression level data obtained by the analysis are, second, fed into the apparatus and compared with the data of the reference data bank obtainable by the above method. For this purpose, the apparatus suitably contains a device for entering the expression level of the data, for example a control panel such as a keyboard. The results, whether and how the data of the unknown sample fit into the reference data bank can be made visible on a provided monitor or display screen and, if desired, printed out on an incorporated or connected printer.

Alternatively, the apparatus of the present invention is equipped with particular appliances suitable for detecting and measuring the expression profile data and, subsequently, proceeding with the comparison with the reference data bank. In this embodiment, the apparatus of the present invention can contain a gripper arm and/or a tray which takes up the microarray containing the hybridized nucleic acids.

In another embodiment, the present invention refers to a reference data bank for distinguishing AML-specific FLT3 length mutations from TKD mutations in a sample obtainable by comprising

- (a) compiling a gene expression profile of a patient sample by determining the expression level of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy ID) as defined in Tables 1, and/or 2, and
- 5 (b) classifying the gene expression profile by means of a machine learning algorithm.

Preferably, the reference data bank is backed up and/or contained in a computational memory data chip.

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The invention is further illustrated in the following table and examples, without limiting the scope of the invention:

TABLES 1.1-2.28

- 15 Tables 1-2 show AML subtype analysis of AML-specific FLT3 length mutations from TKD mutations. The analysed markers are ordered according to their q-values, beginning with the lowest q-values.

For convenience and a better understanding, Tables 1.1 to 2.28 are accompanied with explanatory tables (Table 1.1A to 2.28A) where the numbering and the Affymetrix Id are further defined by other parameters, e.g. gene bank accession number.

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EXAMPLES

- 25 **Example 1: General experimental design of the invention and results**

Different subtypes of acute myeloid leukemia (AML) can clearly be distinguished by morphology, cytogenetics, and molecular genetics. Mutations within the FLT3-gene are the most common genetic alterations in AML. Length mutations in the juxtamembrane domain of FLT3 (FLT3-LM) were detected in 460/2134 (21.6%) and mutations in the tyrosine kinase domain (TKD-mutations) in 98/1711 (5.7%) of newly diagnosed AML in our series. Both kinds of FLT3 mutations can be found most frequently in AML with normal karyotype (AML-NK). While for TKD mutations a prognostic significance has not yet been shown, the FLT3-LM defines a prognostically unfavorable subset of AML-NK. Some of these pts have loss of the wildtype (WT) FLT3 allele in addition to the FLT3-LM. These pts were shown

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to have an even worse outcome than FLT3-LM+ pts that retain the WT-allele. Here we addressed the questions 1) whether pts with FLT3 mutations can be identified from those without FLT3 mutations within the AML-NK and 2) whether different types of FLT3 mutations can be identified by distinct gene expression signatures.

5 Therefore, 148 cases with AML-NK were analyzed by U133 set microarrays (Affymetrix). For each patient the FLT3-LM status was assessed by GeneScan analysis (Applied Biosystems) and the TKD mutation status by melting curve analysis and sequencing. The total cohort was subdivided into 8 groups 1) AML NK and no FLT3 mutation (n=63), 2) status 1: FLT3-LM/WT ratio <0.3 (n=12), 3)

10 status 2: ratio 0.7-1.1 (n=19), 4) status 3: ratio of >1.2=partial loss of WT (n=30), 5) status 4: total loss of WT (n=5), 6) status 5: two or more low status mutations (n=5), 7) TKD mutation (n=10), 8) TKD + LM (n=3). Microarray data was analyzed by pattern recognition algorithms (Principal Component Analysis (PCA) and hierarchical clustering), as well as Support Vector Machines (SVM) for

15 estimation of classification accuracies. Therefore, all samples were divided into a training set consisting of 2/3 of cases to build a SVM model and a test set with remaining 1/3 of cases. Differentially expressed genes were selected according to ANOVA and t-test-statistics in the training set. A specific expression pattern was assessed for each of the defined subgroups. Using pairwise comparisons, the TKD

20 mutations can clearly be distinguished from the FLT3-LM. In addition, FLT3-LM with loss of WT reveal a specific expression pattern in comparison to low status FLT3-LM. By use of SVM comparisons to AML-NK and all other mutation classes an accuracy of 100% was found for status 4, 78% for status 3 (sensitivity 64%, specificity 84%), 74% for status 2 (sensitivity 17%, specificity 88%), 75% for

25 status 1 (sensitivity 50%, specificity 79%), 88% for TKD mutations (sensitivity 50%, specificity 95%), but only 8% for status 5 mutations. In conclusion a high percentage of cases of the different FLT3-mutations can be exactly assigned. Only the status 5 mutations can not be defined by a specific expression profile. Besides their clinical differences we could show that pts with FLT3-LM with different

30 quantitative status of the LM as well as the TKD mutations are also different with regard to their expression pattern. This supports the hypothesis i) that FLT3-LM and TKD mutations act through different downstream target genes and play different functional roles in leukemogenesis; ii) that FLT3-LM cases with loss of the WT-allele should be regarded differently, i.e. with regard to prognosis and

35 therapeutical interventions.

Example 2: General materials, methods and definitions of functional annotations

- 5 The methods section contains both information on statistical analyses used for identification of differentially expressed genes and detailed annotation data of identified microarray probesets.

Affymetrix Probeset Annotation

- 10 All annotation data of GeneChip® arrays are extracted from the NetAffx™ Analysis Center (internet website: www.affymetrix.com). Files for U133 set arrays, including U133A and U133B microarrays are derived from the June 2003 release. The original publication refers to: Liu G, Loraine AE, Shigeta R, Cline M, Cheng J, Valmeekam V, Sun S, Kulp D, Siani-Rose MA. NetAffx: Affymetrix probesets and annotations. Nucleic Acids Res. 2003;31(1):82-6.

- 20 The sequence data are omitted due to their large size, and because they do not change, whereas the annotation data are updated periodically, for example new information on chromosomal location and functional annotation of the respective gene products. Sequence data are available for download in the NetAffx Download Center (www.affymetrix.com)

Data fields:

- 25 In the following section, the content of each field of the data files are described. Microarray probesets, for example found to be differentially expressed between different types of leukemia samples are further described by additional information. The fields are of the following types:

- 30 1. GeneChip Array Information
2. Probe Design Information
3. Public Domain and Genomic References

1. GeneChip Array Information

- 35 HG-U133 ProbeSet_ID:
HG-U133 ProbeSet_ID describes the probe set identifier. Examples are: 200007_at, 200011_s_at, 200012_x_at.

GeneChip:

The description of the GeneChip probe array name where the respective probeset is represented. Examples are: Affymetrix Human Genome U133A Array or
5 Affymetrix Human Genome U133B Array.

2. Probe Design Information**Sequence Type:**

10 The Sequence Type indicates whether the sequence is an Exemplar, Consensus or Control sequence. An Exemplar is a single nucleotide sequence taken directly from a public database. This sequence could be an mRNA or EST. A Consensus sequence, is a nucleotide sequence assembled by Affymetrix, based on one or more
15 sequence taken from a public database.

Transcript ID:

The cluster identification number with a sub-cluster identifier appended.

Sequence Derived From:

20 The accession number of the single sequence, or representative sequence on which the probe set is based. Refer to the "Sequence Source" field to determine the database used.

Sequence ID:

25 For Exemplar sequences: Public accession number or GenBank identifier. For Consensus sequences: Affymetrix identification number or public accession number.

Sequence Source:

30 The database from which the sequence used to design this probe set was taken. Examples are: GenBank®, RefSeq, UniGene, TIGR (annotations from The Institute for Genomic Research).

3. Public Domain and Genomic References

Most of the data in this section come from LocusLink and UniGene databases, and are annotations of the reference sequence on which the probe set is modeled.

5

Gene Symbol and Title:

A gene symbol and a short title, when one is available. Such symbols are assigned by different organizations for different species. Affymetrix annotational data come from the UniGene record. There is no indication which species-specific databank was used, but some of the possibilities include for example HUGO: The Human Genome Organization.

10

MapLocation:

The map location describes the chromosomal location when one is available.

15

Unigene_Accession:

UniGene accession number and cluster type. Cluster type can be "full length" or "est", or "---" if unknown.

20

LocusLink:

This information represents the LocusLink accession number.

Full Length Ref. Sequences:

Indicates the references to multiple sequences in RefSeq. The field contains the ID and description for each entry, and there can be multiple entries per probeSet.

25

Example 3: Sample preparation, processing and data analysis

Method 1:

Microarray analyses were performed utilizing the GeneChip[®] System (Affymetrix, Santa Clara, USA). Hybridization target preparations were performed according to recommended protocols (Affymetrix Technical Manual). In detail, at time of diagnosis, mononuclear cells were purified by Ficoll-Hypaque density centrifugation. They had been lysed immediately in RLT buffer (Qiagen, Hilden, Germany), frozen, and stored at -80°C from 1 week to 38 months. For gene expression profiling cell lysates of the leukemia samples were thawed,

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homogenized (QIAshredder, Qiagen), and total RNA was extracted (RNeasy Mini Kit, Qiagen). Subsequently, 5-10 µg total RNA isolated from 1×10^7 cells was used as starting material for cDNA synthesis with oligo[(dT)₂₄T7promotor]₆₅ primer (cDNA Synthesis System, Roche Applied Science, Mannheim, Germany).
5 cDNA products were purified by phenol/chlorophorm/IAA extraction (Ambion, Austin, USA) and acetate/ethanol-precipitated overnight. For detection of the hybridized target nucleic acid biotin-labeled ribonucleotides were incorporated during the following *in vitro* transcription reaction (Enzo BioArray HighYield RNA Transcript Labeling Kit, Enzo Diagnostics). After quantification by
10 spectrophotometric measurements and 260/280 absorbance values assessment for quality control of the purified cRNA (RNeasy Mini Kit, Qiagen), 15 µg cRNA was fragmented by alkaline treatment (200 mM Tris-acetate, pH 8.2/500 mM potassium acetate/150 mM magnesium acetate) and added to the hybridization cocktail sufficient for five hybridizations on standard GeneChip microarrays (300 µl final
15 volume). Washing and staining of the probe arrays was performed according to the recommended Fluidics Station protocol (EukGE-WS2v4). Affymetrix Microarray Suite software (version 5.0.1) extracted fluorescence signal intensities from each feature on the microarrays as detected by confocal laser scanning according to the manufacturer's recommendations.

20 Expression analysis quality assessment parameters included visual array inspection of the scanned image for the presence of image artifacts and correct grid alignment for the identification of distinct probe cells as well as both low 3'/5' ratio of housekeeping controls (mean: 1.90 for GAPDH) and high percentage of
25 detection calls (mean: 46.3% present called genes). The 3' to 5' ratio of GAPDH probesets can be used to assess RNA sample and assay quality. Signal values of the 3' probe sets for GAPDH are compared to the Signal values of the corresponding 5' probe set. The ratio of the 3' probe set to the 5' probe set is generally no more than 3.0. A high 3' to 5' ratio may indicate degraded RNA or inefficient synthesis
30 of ds cDNA or biotinylated cRNA (GeneChip[®] Expression Analysis Technical Manual, www.affymetrix.com). Detection calls are used to determine whether the transcript of a gene is detected (present) or undetected (absent) and were calculated using default parameters of the Microarray Analysis Suite MAS 5.0 software package.

Method 2:

Bone marrow (BM) aspirates are taken at the time of the initial diagnostic biopsy and remaining material is immediately lysed in RLT buffer (Qiagen), frozen and stored at -80 C until preparation for gene expression analysis. For microarray analysis the GeneChip System (Affymetrix, Santa Clara, CA, USA) is used. The targets for GeneChip analysis are prepared according to the current Expression Analysis. Briefly, frozen lysates of the leukemia samples are thawed, homogenized (QIAshredder, Qiagen) and total RNA extracted (RNeasy Mini Kit, Qiagen). Normally 10 ug total RNA isolated from 1×10^7 cells is used as starting material in the subsequent cDNA-Synthesis using Oligo-dT-T7-Promotor Primer (cDNA synthesis Kit, Roche Molecular Biochemicals). The cDNA is purified by phenol-chlorophorm extraction and precipitated with 100% Ethanol over night. For detection of the hybridized target nucleic acid biotin-labeled ribonucleotides are incorporated during the in vitro transcription reaction (Enzo® BioArray™ HighYield™ RNA Transcript Labeling Kit, ENZO). After quantification of the purified cRNA (RNeasy Mini Kit, Qiagen), 15 ug are fragmented by alkaline treatment (200 mM Tris-acetate, pH 8.2, 500 mM potassium acetate, 150 mM magnesium acetate) and added to the hybridization cocktail sufficient for 5 hybridizations on standard GeneChip microarrays. Before expression profiling Test3 Probe Arrays (Affymetrix) are chosen for monitoring of the integrity of the cRNA. Only labeled cRNA-cocktails which showed a ratio of the measured intensity of the 3' to the 5' end of the GAPDH gene less than 3.0 are selected for subsequent hybridization on HG-U133 probe arrays (Affymetrix). Washing and staining the Probe arrays is performed as described (siehe Affymetrix-Original-Literatur (LOCKHART und LIPSHUTZ). The Affymetrix software (Microarray Suite, Version 4.0.1) extracted fluorescence intensities from each element on the arrays as detected by confocal laser scanning according to the manufacturers recommendations.

Table 1

1. One-Versus-All (OVA)								
1.1	D835 versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	235040_at	DKFZp761H0421	-2.50	2.75E-14	7.95E-10	-0.74	-8.71	17q21.2
2	221809_at	KIAA1464	-3.47	8.72E-14	1.26E-09	-0.69	-8.29	16q21
3	208963_x_at	FADS1	-9.33	4.11E-13	3.97E-09	-0.67	-8.00	11q12.2-q13.1
4	202111_at	SLC4A2	-4.12	1.37E-12	9.92E-09	-0.65	-7.83	7q35-q36
5	208420_x_at	SUPT6H	-1.76	7.94E-09	1.44E-05	-0.69	-7.38	17q11.2
6	219254_at	FLJ22222	-3.09	1.94E-09	4.67E-06	-0.67	-7.33	17q25.3
7	230285_at	DKFZp313A2432	-1.99	1.14E-08	1.93E-05	-0.68	-7.25	11p14.2
8	208791_at	CLU	-6.64	6.52E-11	3.77E-07	-0.59	-7.11	8p21-p12
9	206301_at	TEC	-3.41	1.36E-10	5.64E-07	-0.60	-7.06	4p12
10	236140_at	GCLM	-3.11	1.05E-10	5.08E-07	-0.59	-7.04	1p22.1
11	209179_s_at	LENG4	-2.03	1.01E-06	4.94E-04	-0.75	-6.98	19q13.4
12	215710_at	SIAT4C	-2.21	1.63E-09	4.29E-06	-0.60	-6.91	11q23-q24
13	209739_s_at	DXS1283E	-2.82	1.11E-07	1.02E-04	-0.67	-6.91	Xp22.3
14	213042_s_at	ATP2A3	-3.04	2.15E-10	7.76E-07	-0.58	-6.89	17p13.3
15	200721_s_at	ACTR1A	-1.52	3.70E-07	2.49E-04	-0.70	-6.88	10q24.32
16	206494_s_at	ITGA2B	-4.84	7.51E-10	2.17E-06	-0.59	-6.87	17q21.32
17	238959_at	LOC113251	-2.37	1.15E-07	1.02E-04	-0.66	-6.79	12q13.12
18	225233_at		-3.31	6.66E-10	2.14E-06	-0.57	-6.77	
19	226445_s_at	TRIM41	-1.34	1.05E-06	5.06E-04	-0.65	-6.42	5q35.3
20	224851_at		-2.15	2.23E-07	1.61E-04	-0.61	-6.41	
21	208996_s_at	POLR2C	-1.43	1.36E-05	3.01E-03	-0.77	-6.35	16q13-q21
22	227669_at		-1.60	2.48E-06	9.07E-04	-0.67	-6.35	
23	208962_s_at	FADS1	-2.68	1.23E-06	5.83E-04	-0.64	-6.33	11q12.2-q13.1
24	209392_at	ENPP2	-3.31	7.28E-09	1.40E-05	-0.54	-6.33	8q24.1
25	218832_x_at	ARRB1	-2.78	3.13E-09	6.96E-06	-0.53	-6.32	11q13
26	205227_at	IL1RAP	-2.79	1.79E-07	1.40E-04	-0.59	-6.32	3q28
27	223176_at	MGC14254	-2.30	1.03E-05	2.53E-03	-0.73	-6.29	6p21.2
28	208756_at	EIF3S2	-1.32	1.06E-05	2.57E-03	-0.73	-6.27	1p34.1
29	233013_x_at		-1.36	8.92E-08	8.60E-05	-0.57	-6.27	
30	202427_s_at	DKFZP564B167	-1.50	1.33E-05	2.99E-03	-0.74	-6.26	1q24
31	243631_at		-1.77	2.19E-07	1.61E-04	-0.58	-6.26	
32	226282_at		-19.14	5.34E-09	1.10E-05	-0.53	-6.24	
33	210571_s_at	CMAH	-2.06	2.26E-06	8.65E-04	-0.64	-6.23	6p21.32
34	212968_at	RFNG	-1.42	4.69E-07	2.95E-04	-0.59	-6.18	17q25
35	223364_s_at	DDX37	-2.90	5.73E-06	1.58E-03	-0.67	-6.18	12q24.31
36	222425_s_at	DKFZP586F1524	-2.47	3.48E-06	1.17E-03	-0.64	-6.14	17q11.1
37	213800_at	HF1	-3.68	3.74E-08	4.92E-05	-0.54	-6.14	1q32
38	202974_at	MPP1	-1.62	1.16E-07	1.02E-04	-0.55	-6.09	Xq28

39	204379_s_at	FGFR3	-3.29	1.23E-08	1.97E-05	-0.50	-6.06	4p16.3
40	36936_at	TSTA3	-1.71	2.41E-07	1.70E-04	-0.55	-6.05	8q24.3
41	201932_at	MUF1	-2.07	1.61E-05	3.31E-03	-0.70	-6.04	1p33
42	214446_at	ELL2	-3.57	1.56E-08	2.38E-05	-0.50	-6.02	5q14.3
43	213983_s_at	KIAA0648	-1.68	1.95E-06	7.94E-04	-0.60	-6.02	4p14
44	221499_s_at	NPEPL1	-1.55	1.61E-05	3.31E-03	-0.69	-6.02	20q13.32
45	228278_at		-2.71	7.75E-07	4.40E-04	-0.57	-6.02	
46	223818_s_at	HBXAP	-2.74	4.21E-06	1.33E-03	-0.62	-6.01	11q13.3
47	210233_at	IL1RAP	-2.88	5.03E-08	5.39E-05	-0.52	-6.01	3q28
48	204936_at	MAP4K2	-2.84	1.72E-07	1.38E-04	-0.54	-5.99	11q13
49	212100_s_at	KIAA1649	-1.26	2.57E-06	9.16E-04	-0.60	-5.98	22q13.2
50	202593_s_at	MIR16	-1.74	1.86E-06	7.86E-04	-0.59	-5.97	16p12-p11.2
1.2	Double versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	220623_s_at	TSGA10	2.18	2.21E-16	2.82E-13	1.85	20.39	2q11.2
2	205282_at	LRP8	1.75	1.29E-12	5.85E-10	1.49	16.19	1p34
3	214037_s_at	JM1	1.74	9.30E-13	4.42E-10	1.48	16.05	Xp11.23
4	219938_s_at	PSTPIP2	1.70	5.86E-30	2.40E-25	1.35	16.02	18q12
5	200595_s_at	EIF3S10	1.45	9.39E-11	2.63E-08	1.49	15.75	10q26
6	209476_at	TXNDC	1.69	1.86E-14	1.32E-11	1.40	15.49	14q21.3
7	201382_at	SIP	1.91	1.69E-06	1.21E-04	1.64	15.32	1q24-q25
8	213053_at	KIAA0841	1.55	6.33E-16	7.19E-13	1.33	14.99	19q13.11
9	205424_at	ProSAPIP2	-3.49	7.76E-28	1.59E-23	-1.20	-14.36	17q21.32
10	218109_s_at	FLJ14153	1.63	2.34E-11	7.71E-09	1.29	13.95	3q25.32
11	222583_s_at	NUP50	1.73	2.35E-18	6.02E-15	1.20	13.83	22q13.31
12	202462_s_at	KIAA0801	1.56	3.90E-08	4.76E-06	1.35	13.73	5q31.1
13	222779_s_at	HSA277841	1.63	5.17E-05	2.14E-03	1.58	13.44	17p13.3
14	214092_x_at	SFRS14	1.42	1.30E-21	7.59E-18	1.13	13.29	19p12
15	232075_at	REC14	1.90	5.08E-05	2.12E-03	1.53	13.15	15q24.1
16	200809_x_at	RPL12	-1.18	3.19E-22	2.17E-18	-1.10	-12.96	9q34
17	217746_s_at	PDCD6IP	1.41	1.51E-17	2.46E-14	1.11	12.82	3p22.1
18	229812_at	FLJ23277	1.62	1.12E-06	8.50E-05	1.31	12.74	1p36.12
19	202228_s_at	SDFR1	1.70	2.59E-10	6.26E-08	1.18	12.71	15q22
20	208700_s_at	TKT	1.54	1.83E-10	4.63E-08	1.17	12.65	3p14.3
21	244180_at		-5.42	7.81E-25	8.68E-21	-1.04	-12.57	
22	208064_s_at	SIAT8C	-5.13	3.66E-16	4.40E-13	-1.09	-12.54	18q21.2
23	241086_at		-3.99	8.49E-25	8.68E-21	-1.04	-12.54	
24	209206_at	SEC22L1	1.42	6.26E-21	2.85E-17	1.04	12.30	1q21.2-q21.3
25	241330_x_at		-7.94	2.29E-23	1.87E-19	-1.02	-12.28	
26	201784_s_at	SMAP	1.38	1.43E-13	8.01E-11	1.09	12.28	11p15.1
27	202306_at	POLR2G	1.52	1.33E-05	6.94E-04	1.33	12.17	11q13.1
28	208374_s_at	CAPZA1	1.47	2.47E-06	1.66E-04	1.25	12.06	1p13.1

29	222673_x_at	LOC159090	1.59	6.03E-06	3.56E-04	1.26	11.88	Xq26.3
30	203983_at	TSNAX	1.74	2.55E-05	1.20E-03	1.27	11.55	1q42.1
31	221471_at	TDE1	1.58	8.25E-11	2.36E-08	1.04	11.40	20q13.1-13.3
32	218538_s_at	MRS2L	1.69	9.92E-06	5.43E-04	1.21	11.38	6p22.3-p22.1
33	232612_s_at	FLJ10035	-2.05	2.46E-21	1.26E-17	-0.95	-11.36	2q37.1
34	213911_s_at	H2AFZ	1.37	5.73E-05	2.32E-03	1.28	11.31	4q24
35	201464_x_at	JUN	1.78	9.29E-07	7.30E-05	1.13	11.28	1p32-p31
36	227442_at	FLJ38991	1.40	6.88E-15	5.52E-12	0.97	11.14	4q13.3
37	238673_at		-2.39	1.17E-17	2.08E-14	-0.95	-11.13	
38	210830_s_at	PON2	-2.93	1.61E-20	6.59E-17	-0.92	-11.08	7q21.3
39	215424_s_at	SNW1	1.27	3.03E-20	1.03E-16	0.92	11.05	14q24.3
40	236803_at	NBR2	-5.13	2.27E-12	9.59E-10	-0.96	-10.86	17q21
41	204798_at	MYB	1.62	6.88E-07	5.69E-05	1.08	10.85	6q22-q23
42	218243_at	RUFY1	1.37	1.65E-08	2.24E-06	1.02	10.83	5q35.3
43	201909_at	RPS4Y	-28.68	3.00E-20	1.03E-16	-0.90	-10.80	Yp11.3
44	205360_at	PFDN4	-3.89	5.24E-10	1.18E-07	-0.99	-10.78	20q13
45	236371_s_at	NCOA6IP	-2.69	3.66E-20	1.15E-16	-0.89	-10.77	8q11
46	204082_at	PBX3	1.63	1.03E-17	1.98E-14	0.91	10.74	9q33-q34
47	207764_s_at	HIPK3	1.49	2.64E-16	3.28E-13	0.92	10.72	11p13
48	203445_s_at	OS4	-1.34	8.70E-20	2.54E-16	-0.89	-10.66	12q13-q15
49	219600_s_at	C21orf4	1.62	3.00E-05	1.37E-03	1.16	10.65	21q22.11
50	213737_x_at		1.50	2.58E-06	1.72E-04	1.07	10.58	
1.3	Status 1 versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	217246_s_at	EPAG	-3.11	8.86E-08	2.19E-04	-0.73	-7.19	X
2	205013_s_at	ADORA2A	-1.98	7.26E-09	5.37E-05	-0.61	-6.79	22q11.23
3	217450_at		-2.14	8.12E-10	1.57E-05	-0.56	-6.65	
4	237243_at		-3.06	1.22E-08	7.41E-05	-0.59	-6.62	
5	220363_s_at	ELMO2	-3.43	1.47E-09	1.57E-05	-0.54	-6.51	20q13
6	208145_at	FLJ20802	-2.72	1.70E-09	1.57E-05	-0.54	-6.48	20p13
7	229262_at		-2.83	1.52E-09	1.57E-05	-0.54	-6.48	
8	218059_at	LOC51123	-1.45	6.64E-08	1.76E-04	-0.60	-6.46	8q22.3
9	204383_at	DGCR14	-1.55	4.98E-06	2.71E-03	-0.74	-6.35	22q11.21
10	242713_at		-2.09	6.22E-08	1.76E-04	-0.58	-6.32	
11	214266_s_at	ENIGMA	-2.42	2.38E-08	9.78E-05	-0.55	-6.29	5q35.3
12	211523_at	GNRHR	-2.98	2.96E-06	2.03E-03	-0.67	-6.20	4q21.2
13	223441_at	SLC17A5	-1.89	1.40E-08	7.41E-05	-0.53	-6.19	6q14-q15
14	227045_at		-1.51	6.62E-08	1.76E-04	-0.56	-6.19	
15	238785_at		-1.51	1.91E-08	8.85E-05	-0.52	-6.09	
16	213244_at	SCAMP-4	-1.76	9.15E-07	9.96E-04	-0.58	-5.99	19p13.3
17	206730_at	GRIA3	-2.63	3.28E-08	1.22E-04	-0.49	-5.85	Xq25-q26
18	228812_at		-1.99	2.95E-06	2.03E-03	-0.59	-5.84	

19	210260_s_at	GG2-1	-1.67	2.18E-07	4.24E-04	-0.52	-5.84	5q23.1
20	209898_x_at	ITSN2	-1.62	2.54E-07	4.48E-04	-0.52	-5.83	2pter-p25.1
21	233888_s_at	SRGAP1	-2.47	3.16E-07	5.08E-04	-0.53	-5.83	12q14.1
22	201110_s_at	THBS1	-5.55	4.77E-08	1.61E-04	-0.48	-5.77	15q15
23	224230_at	IL1F8	-2.30	3.51E-07	5.20E-04	-0.51	-5.74	2q12-q14.1
24	205633_s_at	ALAS1	-2.02	3.39E-07	5.20E-04	-0.51	-5.69	3p21.1
25	201369_s_at	ZFP36L2	-2.07	3.21E-06	2.09E-03	-0.55	-5.63	2p22.3-p21
26	204614_at	SERPINB2	-4.71	9.95E-08	2.30E-04	-0.47	-5.62	18q21.3
27	223346_at	VPS18	-1.65	8.03E-06	3.50E-03	-0.59	-5.61	15q14-q15
28	226566_at	TRIM11	-1.55	1.65E-06	1.52E-03	-0.52	-5.58	1q42.13
29	212117_at	TC10	-1.55	2.29E-06	1.73E-03	-0.53	-5.58	2p21
30	240943_at		-2.15	1.43E-06	1.46E-03	-0.52	-5.56	
31	213033_s_at		-1.99	2.15E-07	4.24E-04	-0.47	-5.56	
32	216982_x_at		-2.93	1.44E-07	3.15E-04	-0.46	-5.55	
33	235705_at		-2.15	6.09E-07	8.05E-04	-0.49	-5.54	
34	234952_s_at	KIAA1542	-1.93	1.01E-05	4.02E-03	-0.57	-5.49	11p15.5
35	207082_at	CSF1	-1.99	5.24E-07	7.18E-04	-0.48	-5.48	1p21-p13
36	216180_s_at		-3.49	2.30E-07	4.26E-04	-0.46	-5.47	
37	204965_at	GC	-2.50	7.45E-07	8.73E-04	-0.48	-5.46	4q12-q13
38	201460_at	MAPKAPK2	-1.47	1.35E-05	4.80E-03	-0.57	-5.44	1q32
39	239334_at		-2.59	1.58E-06	1.52E-03	-0.49	-5.42	
40	222383_s_at	ALOXE3	-1.93	2.69E-07	4.52E-04	-0.45	-5.41	17p13.1
41	223596_at	SLC12A6	-1.73	6.77E-07	8.64E-04	-0.47	-5.39	15q13-q15
42	240949_x_at		-2.33	5.28E-06	2.76E-03	-0.52	-5.38	
43	203045_at	NINJ1	-2.30	1.33E-06	1.41E-03	-0.48	-5.37	9q22
44	211030_s_at	SLC6A6	-5.12	3.98E-07	5.66E-04	-0.44	-5.32	3p25-p24
45	224669_at	C20orf169	-1.32	1.74E-05	5.37E-03	-0.56	-5.31	20q13.11
46	207742_s_at	NR6A1	-1.80	5.86E-06	2.80E-03	-0.51	-5.30	9q33-q34.1
47	216672_s_at	MYT1L	-2.40	7.25E-07	8.73E-04	-0.45	-5.30	2p25.3
48	211411_at		-2.31	1.80E-06	1.62E-03	-0.47	-5.29	
49	221697_at		-2.20	6.05E-06	2.84E-03	-0.51	-5.29	
50	227539_at	GNA13	-1.90	8.93E-06	3.76E-03	-0.52	-5.27	17q24.3
1.4	Status 2 versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	228423_at		-1.95	6.99E-06	8.80E-02	-0.44	-4.88	
2	205372_at	PLAG1	-2.63	4.35E-06	8.80E-02	-0.41	-4.84	8q12
3	229963_at		-3.45	6.20E-06	8.80E-02	-0.41	-4.76	
4	230341_x_at	ADAMTS10	-1.56	1.14E-05	9.44E-02	-0.43	-4.74	19p13.2
5	236522_at		-1.47	1.25E-05	9.44E-02	-0.40	-4.62	
6	214462_at	SOCS4	-1.51	7.60E-05	2.31E-01	-0.50	-4.59	18q22.2
7	234216_at		-1.48	3.15E-05	1.68E-01	-0.42	-4.55	
8	220145_at	FLJ21159	-3.36	1.92E-05	1.21E-01	-0.37	-4.42	4q31.3
9	203854_at	IF	-2.01	3.56E-05	1.68E-01	-0.37	-4.31	4q25

10	202967_at	GSTA4	-1.35	9.19E-05	2.32E-01	-0.40	-4.25	6p12.1
11	215139_at		1.96	3.50E-04	3.00E-01	0.57	4.24	
12	207472_at	PRO1992	-2.56	8.58E-05	2.31E-01	-0.38	-4.19	6q15
13	215487_x_at		-1.92	1.39E-04	2.83E-01	-0.40	-4.17	
14	229563_s_at	RPL10A	-1.13	8.06E-05	2.31E-01	-0.37	-4.16	6p21.3-p21.2
15	212151_at		-2.20	1.25E-04	2.78E-01	-0.39	-4.15	
16	206363_at	MAF	-2.86	7.74E-05	2.31E-01	-0.35	-4.12	16q22-q23
17	226682_at		-2.50	7.42E-05	2.31E-01	-0.34	-4.08	
18	220296_at	FLJ11715	-1.60	2.02E-04	2.83E-01	-0.40	-4.08	5q33.2
19	212843_at	NCAM1	-2.81	7.73E-05	2.31E-01	-0.34	-4.07	11q23.1
20	202972_s_at	FAM13A1	-1.27	1.81E-04	2.83E-01	-0.39	-4.06	4q22.1
21	237942_at	SNRK	-1.53	3.57E-04	3.00E-01	-0.45	-4.05	3p21.32
22	218409_s_at	DNAJC1	1.44	4.39E-04	3.43E-01	0.47	4.03	10p12.31
23	240349_at		-1.94	1.22E-04	2.78E-01	-0.35	-4.02	
24	232341_x_at	HABP4	-1.40	1.83E-04	2.83E-01	-0.37	-4.01	9q22.3-q31
25	200021_at - HG-U133B	CFL1	-1.12	2.41E-04	2.84E-01	-0.38	-3.99	11q13
26	234809_at	HCA127	-1.93	2.10E-04	2.83E-01	-0.37	-3.98	Xq11.1
27	200099_s_at - HG-U133B		-1.13	1.80E-04	2.83E-01	-0.36	-3.98	
28	200032_s_at - HG-U133B	RPL9	-1.10	1.97E-04	2.83E-01	-0.36	-3.97	4p13
29	217558_at	CYP2C9	-1.38	2.13E-04	2.83E-01	-0.36	-3.95	10q24
30	241435_at		-1.72	1.55E-04	2.83E-01	-0.34	-3.93	
31	200014_s_at - HG-U133B	HNRPC	1.21	5.96E-04	3.75E-01	0.45	3.90	14q11.1
32	240555_at		-1.75	2.30E-04	2.83E-01	-0.35	-3.90	
33	240568_at		-1.52	2.13E-04	2.83E-01	-0.35	-3.90	
34	206694_at	PNLIPRP1	-1.74	1.85E-04	2.83E-01	-0.34	-3.89	10q26.11
35	242995_at		-1.51	5.61E-04	3.72E-01	-0.43	-3.89	
36	222379_at		-1.92	3.54E-04	3.00E-01	-0.38	-3.88	
37	204793_at	KIAA0443	-1.87	2.20E-04	2.83E-01	-0.34	-3.86	Xq22.1
38	221715_at		-1.98	2.97E-04	2.98E-01	-0.35	-3.83	
39	AFFX-BioDn-3_at - HG-U133B		-1.16	2.69E-04	2.90E-01	-0.34	-3.83	
40	222984_at	PAIP2	1.17	6.26E-04	3.76E-01	0.42	3.83	5q31.3
41	211682_x_at	UGT2B28	-1.70	2.32E-04	2.83E-01	-0.33	-3.82	4q13.3
42	241808_at		-2.35	2.65E-04	2.90E-01	-0.34	-3.82	
43	243542_at		-2.14	3.13E-04	3.00E-01	-0.34	-3.80	
44	228003_at		-1.42	3.28E-04	3.00E-01	-0.34	-3.79	
45	227935_s_at	MGC16202	-1.43	4.45E-04	3.43E-01	-0.36	-3.79	10q23.32
46	213954_at	KIAA0888	-1.99	2.77E-04	2.91E-01	-0.33	-3.78	5q13.2
47	233271_at		-1.34	4.80E-04	3.59E-01	-0.36	-3.76	
48	205495_s_at	GNLY	-2.35	2.63E-04	2.90E-01	-0.31	-3.75	2p12-q11
49	203830_at	NJMU-R1	1.60	1.16E-03	4.31E-01	0.51	3.75	17q11.2
50	222702_x_at	CRIP1	1.44	1.24E-03	4.35E-01	0.50	3.72	2p21
1.5	Status 3 versus rest							

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	211396_at	FCGR2B	-2.71	1.56E-09	3.46E-05	-0.54	-6.47	1q23
2	237169_at		-2.81	4.03E-09	4.23E-05	-0.52	-6.27	
3	203214_x_at	CDC2	-1.92	5.72E-09	4.23E-05	-0.52	-6.23	10q21.1
4	209301_at	CA2	-2.58	1.02E-08	4.46E-05	-0.51	-6.11	8q22
5	239327_at		-3.72	1.04E-08	4.46E-05	-0.51	-6.09	
6	239413_at		-1.64	1.41E-08	4.46E-05	-0.51	-6.07	
7	217683_at		-3.00	2.57E-08	5.66E-05	-0.52	-6.03	
8	218726_at	DKFZp762E1312	-2.23	1.39E-08	4.46E-05	-0.50	-6.02	2q37.1
9	242496_at		-2.17	1.66E-08	4.61E-05	-0.50	-5.98	
10	205592_at	SLC4A1	-4.66	2.48E-08	5.66E-05	-0.49	-5.91	17q21-q22
11	56748_at	TRIM10	-1.71	3.13E-08	5.79E-05	-0.49	-5.89	6p21.3
12	208416_s_at	SPTB	-5.37	2.81E-08	5.66E-05	-0.49	-5.88	14q23-q24.2
13	210559_s_at	CDC2	-2.00	4.24E-08	7.23E-05	-0.49	-5.83	10q21.1
14	226944_at	HTRA3	-1.85	1.14E-07	1.26E-04	-0.51	-5.77	4p16.1
15	213344_s_at	H2AFX	-1.38	7.83E-08	9.65E-05	-0.49	-5.77	11q23.2-q23.3
16	236305_at	LOC317671	-1.83	5.54E-08	7.89E-05	-0.48	-5.74	
17	211034_s_at	KIAA0614	-1.53	5.67E-08	7.89E-05	-0.48	-5.73	12q24.12
18	209735_at	ABCG2	-1.80	5.69E-08	7.89E-05	-0.48	-5.73	4q22
19	242245_at		-2.05	6.56E-08	8.57E-05	-0.47	-5.71	
20	232278_s_at	FLJ20354	-2.14	1.04E-07	1.22E-04	-0.47	-5.62	1p31.2
21	237336_at	ADD2	-2.17	2.16E-07	1.88E-04	-0.48	-5.59	2p14-p13
22	229610_at	FLJ40629	-1.81	1.78E-07	1.72E-04	-0.48	-5.57	2q13
23	241060_x_at		-2.69	1.76E-07	1.72E-04	-0.46	-5.51	
24	235796_at		-1.67	1.89E-07	1.75E-04	-0.46	-5.50	
25	241859_at		-2.31	1.78E-07	1.72E-04	-0.46	-5.49	
26	206834_at	HBD	-2.10	2.93E-07	2.09E-04	-0.47	-5.49	11p15.5
27	207252_at	INE1	-1.94	5.04E-07	2.68E-04	-0.49	-5.48	Xp11.4-p11.3
28	237207_at		-3.56	2.30E-07	1.89E-04	-0.46	-5.46	
29	205198_s_at	ATP7A	-1.48	2.92E-07	2.09E-04	-0.47	-5.46	Xq13.2-q13.3
30	205631_at	KIAA0586	-1.29	8.22E-07	3.13E-04	-0.50	-5.46	14q22.3
31	218904_s_at	FLJ10110	-2.11	2.20E-07	1.88E-04	-0.45	-5.44	9q21.13
32	203124_s_at	SLC11A2	-1.92	7.40E-07	3.03E-04	-0.49	-5.41	12q13
33	232313_at	DKFZp761O2018	-1.74	2.66E-07	2.09E-04	-0.45	-5.41	12q24.32
34	220886_at	GABRQ	-1.41	3.12E-07	2.13E-04	-0.45	-5.40	Xq28
35	229654_at		-1.79	5.29E-07	2.68E-04	-0.47	-5.39	
36	241807_x_at		-2.27	5.20E-07	2.68E-04	-0.47	-5.39	
37	226179_at		-2.51	2.89E-07	2.09E-04	-0.45	-5.39	
38	241538_at		-2.16	3.16E-07	2.13E-04	-0.45	-5.37	
39	210325_at	CD1A	-1.52	8.44E-07	3.13E-04	-0.48	-5.36	1q22-q23
40	229555_at	GALNT5	-1.69	5.32E-07	2.68E-04	-0.46	-5.35	2q24.1
41	201059_at	EMS1	-1.91	3.46E-07	2.26E-04	-0.44	-5.35	11q13
42	232286_at		-1.90	6.22E-07	2.80E-04	-0.47	-5.35	

43	231274_s_at	MSCP	-2.31	3.62E-07	2.30E-04	-0.44	-5.34	8p21.2
44	203999_at	SYT1	-1.39	5.83E-07	2.80E-04	-0.46	-5.33	12cen-q21
45	211896_s_at	DCN	-1.93	4.20E-07	2.52E-04	-0.45	-5.33	12q13.2
46	218009_s_at	PRC1	-1.54	4.69E-07	2.68E-04	-0.45	-5.33	15q26.1
47	236574_at		-1.45	1.19E-06	3.70E-04	-0.49	-5.33	
48	206468_s_at	CGI-01	-1.47	8.45E-07	3.13E-04	-0.47	-5.32	1q24-q25.3
49	203116_s_at	FECH	-2.46	4.12E-07	2.52E-04	-0.44	-5.31	18q21.3
50	218675_at	BOCT	-2.06	5.65E-07	2.79E-04	-0.45	-5.29	14q11.2
1.6	Status 4 versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	222753_s_at	FLJ22649	-2.05	3.95E-12	2.05E-09	-1.16	-12.34	4q34.2
2	216117_at		-3.02	5.88E-21	5.49E-17	-1.04	-12.28	
3	217239_x_at		-8.06	4.01E-22	8.21E-18	-0.96	-11.54	
4	219251_s_at	FLJ10300	2.44	9.19E-06	2.97E-04	1.48	11.51	7q36.3
5	214344_at	LOC92973	-6.00	5.86E-22	8.21E-18	-0.95	-11.47	9p13.1
6	201536_at	DUSP3	1.60	4.51E-15	7.01E-12	0.99	11.17	17q21
7	238109_at		2.27	1.09E-07	7.86E-06	1.17	11.07	
8	201242_s_at	ATP1B1	2.08	5.12E-07	2.74E-05	1.17	10.70	1q22-q25
9	202371_at	FLJ21174	1.75	6.60E-07	3.38E-05	1.17	10.62	Xq22.1
10	239652_at		-3.48	1.85E-13	1.48E-10	-0.94	-10.57	
11	204895_x_at	MUC4	-3.79	4.64E-19	3.07E-15	-0.88	-10.53	3q29
12	36545_s_at	KIAA0542	1.64	8.18E-06	2.70E-04	1.29	10.51	22q12.2
13	214677_x_at	IGLJ3	-6.38	1.98E-17	6.91E-14	-0.89	-10.48	22q11.1-q11.2
14	215946_x_at	LOC91316	-2.75	5.48E-19	3.07E-15	-0.86	-10.31	22q11.21
15	215943_at	KIAA1661	-4.21	7.97E-17	2.23E-13	-0.88	-10.29	
16	220530_at		-4.33	1.19E-13	1.07E-10	-0.91	-10.25	
17	214836_x_at	IGKC	-4.30	6.47E-17	2.01E-13	-0.86	-10.15	2p12
18	211838_x_at	PCDHA5	-3.99	1.72E-13	1.42E-10	-0.89	-10.11	5q31
19	201022_s_at	DSTN	1.60	2.04E-06	8.44E-05	1.13	10.07	20p11.23
20	242810_x_at		-4.64	3.55E-12	1.87E-09	-0.91	-10.06	
21	221671_x_at	IGKC	-4.89	2.55E-13	1.98E-10	-0.89	-10.05	2p12
22	204939_s_at	PLN	-3.76	1.65E-11	6.59E-09	-0.91	-10.03	6q22.1
23	202404_s_at	COL1A2	-5.99	1.56E-15	3.98E-12	-0.86	-10.02	7q22.1
24	243072_at		-4.49	5.16E-18	2.41E-14	-0.83	-9.98	
25	219595_at	ZNF26	1.34	5.21E-15	7.30E-12	0.85	9.90	12q24.33
26	216573_at		-4.12	1.32E-17	5.29E-14	-0.82	-9.86	
27	213851_at		-2.43	9.59E-07	4.55E-05	-1.05	-9.72	
28	221651_x_at	IGKC	-4.60	3.31E-11	1.16E-08	-0.88	-9.64	2p12
29	219059_s_at	XLKD1	-3.25	1.34E-13	1.13E-10	-0.83	-9.51	11p15
30	234414_at	DKFZp43411117	-2.18	3.50E-15	5.99E-12	-0.81	-9.51	9q22.31
31	217157_x_at	IGKC	-4.80	1.83E-10	4.21E-08	-0.87	-9.46	2p12
32	210824_at	STOM	-3.47	2.65E-14	2.97E-11	-0.81	-9.45	9q34.1

33	220761_s_at	JK	1.49	4.55E-08	3.86E-06	0.93	9.39	12q
34	211897_s_at	CRHR1	-3.91	3.12E-09	4.36E-07	-0.88	-9.30	17q12-q22
35	212608_s_at		1.75	1.55E-04	2.91E-03	1.42	9.28	
36	211302_s_at	PDE4B	-3.12	2.85E-11	1.08E-08	-0.84	-9.28	1p31
37	219964_at	ST7L	2.10	2.40E-05	6.40E-04	1.14	9.20	1p13.1
38	230864_at	MGC42105	-2.51	1.74E-08	1.74E-06	-0.89	-9.20	5p11
39	217688_at	ADCY2	-2.71	4.10E-14	4.25E-11	-0.79	-9.20	5p15.3
40	221005_s_at	PTDSS2	1.85	2.44E-05	6.50E-04	1.13	9.16	11p15
41	235549_at	LOC255488	-6.90	2.97E-15	5.93E-12	-0.77	-9.15	6p22.3
42	204909_at	DDX6	-1.72	2.63E-09	3.81E-07	-0.86	-9.10	11q23.3
43	220941_s_at	C21orf91	-1.66	3.29E-11	1.16E-08	-0.82	-9.10	21q21.1
44	206727_at	C9	-3.63	1.95E-15	4.54E-12	-0.76	-9.09	5p14-p12
45	213926_s_at	HRB	-3.19	5.44E-09	6.85E-07	-0.86	-9.06	2q36
46	215733_x_at	CTAG2	-1.74	5.06E-12	2.53E-09	-0.80	-9.05	Xq28
47	223280_x_at	MS4A6A	-6.39	2.85E-15	5.93E-12	-0.75	-9.00	11q12.1
48	225178_at	FLJ00166	1.85	1.16E-05	3.59E-04	1.05	8.99	3q27.2
49	209138_x_at	IGLJ3	-6.90	3.64E-15	5.99E-12	-0.75	-8.98	22q11.1-q11.2
50	211430_s_at	IGHG3	-9.99	3.53E-15	5.99E-12	-0.74	-8.91	14q32.33
1.7	Status 5 versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	206204_at	GRB14	-5.61	3.50E-20	1.24E-15	-0.91	-10.93	2q22-q24
2	208007_at		-3.83	6.56E-13	1.55E-09	-0.92	-10.19	
3	238067_at	FLJ20298	-12.46	4.24E-17	7.49E-13	-0.80	-9.59	Xq22.2
4	219065_s_at	CGI-27	1.29	1.51E-12	3.13E-09	0.85	9.50	2p23.1
5	203453_at	SCNN1A	-2.94	7.73E-14	2.73E-10	-0.82	-9.46	12p13
6	244854_at		-4.38	8.32E-13	1.84E-09	-0.82	-9.33	
7	214668_at	C13orf1	-2.79	3.31E-10	4.05E-07	-0.83	-8.93	13q14
8	243322_at		-4.21	3.99E-08	1.62E-05	-0.89	-8.92	
9	216978_x_at		-3.25	4.34E-15	5.11E-11	-0.74	-8.88	
10	219736_at	TRIM36	-7.66	2.50E-14	1.39E-10	-0.75	-8.86	5q22.2
11	216661_x_at	CYP2C9	-1.74	1.03E-14	9.07E-11	-0.74	-8.83	10q24
12	208801_at	SRP72	1.20	6.46E-12	1.20E-08	0.77	8.77	4q11
13	210115_at	RPL39L	-5.45	3.25E-14	1.43E-10	-0.73	-8.70	3q27
14	206159_at	GDF10	-3.12	8.12E-07	1.43E-04	-0.92	-8.57	10q11.21
15	233836_at		-2.73	2.75E-14	1.39E-10	-0.71	-8.53	
16	205487_s_at	TONDU	-4.85	2.07E-14	1.39E-10	-0.71	-8.53	Xq26.3
17	206294_at	HSD3B2	-3.07	2.69E-09	1.79E-06	-0.80	-8.51	1p13.1
18	243132_at		-3.47	4.76E-14	1.87E-10	-0.71	-8.49	
19	231010_at	PRO0971	-1.86	2.59E-09	1.76E-06	-0.79	-8.46	4q25
20	204337_at		-3.00	1.21E-07	3.61E-05	-0.85	-8.42	
21	214981_at		-5.33	5.16E-13	1.40E-09	-0.71	-8.35	
22	215086_at	IBTK	-5.68	1.47E-13	4.71E-10	-0.70	-8.32	6q14.3

23	244692_at	FLJ39501	-4.63	3.19E-09	2.01E-06	-0.77	-8.30	19p13.11
24	215323_at		-2.96	2.87E-12	5.63E-09	-0.71	-8.30	
25	231380_at	VEST1	-4.21	1.68E-11	2.70E-08	-0.72	-8.26	8q13
26	202008_s_at	NID	-2.44	3.69E-10	4.35E-07	-0.74	-8.21	1q43
27	207052_at	HAVCR1	-2.69	2.97E-06	3.81E-04	-0.89	-8.06	5q33.2
28	214893_x_at	HCN2	-3.21	5.14E-13	1.40E-09	-0.67	-8.01	19p13.3
29	229894_s_at	KIAA1160	-1.74	8.79E-10	8.17E-07	-0.72	-7.94	3q21.3
30	238933_at	IRS1	-4.11	6.15E-13	1.55E-09	-0.66	-7.92	2q36
31	205879_x_at	RET	-1.96	8.86E-07	1.53E-04	-0.82	-7.90	10q11.2
32	220542_s_at	PLUNC	-2.12	3.66E-06	4.44E-04	-0.87	-7.88	20q11.2
33	203673_at	TG	-2.29	8.50E-06	8.16E-04	-0.90	-7.84	8q24.2-q24.3
34	209742_s_at	MYL2	-2.19	5.67E-11	8.34E-08	-0.68	-7.83	12q23-q24.3
35	211856_x_at	CD28	-2.93	4.17E-08	1.68E-05	-0.74	-7.79	2q33
36	214823_at	ZNF204	-2.28	3.61E-09	2.21E-06	-0.70	-7.66	6p21.3
37	220636_at	DNAI2	-3.24	6.74E-09	3.50E-06	-0.70	-7.65	17q25
38	244858_at		-3.21	1.20E-11	2.02E-08	-0.65	-7.64	
39	206800_at	MTHFR	-2.56	4.91E-11	7.54E-08	-0.65	-7.59	1p36.3
40	230982_at		-3.64	1.61E-05	1.31E-03	-0.88	-7.55	
41	241909_at		-6.31	8.15E-12	1.44E-08	-0.63	-7.52	
42	239567_at		-3.50	2.15E-06	3.01E-04	-0.79	-7.51	
43	211466_at	NFIB	-4.12	4.01E-10	4.57E-07	-0.65	-7.43	9p24.1
44	208061_at	LOC51045	-3.55	3.44E-08	1.43E-05	-0.69	-7.40	
45	221109_at	DKFZp434C0923	-2.50	3.93E-09	2.35E-06	-0.66	-7.38	1q42.13
46	235526_at		-3.04	1.16E-06	1.90E-04	-0.75	-7.37	
47	240691_at		-4.05	2.00E-10	2.62E-07	-0.63	-7.34	
48	207952_at	IL5	-3.22	2.40E-08	1.07E-05	-0.67	-7.29	5q31.1
49	215270_at	LFNG	-3.00	4.14E-10	4.57E-07	-0.63	-7.28	7p22
50	239286_at		-3.55	5.66E-06	6.17E-04	-0.78	-7.27	
1.8	normal versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	209014_at	MAGED1	-1.82	1.05E-10	1.88E-06	-0.61	-7.12	Xp11.23
2	235391_at	LOC137392	-2.57	1.29E-10	1.88E-06	-0.61	-7.08	8q21.3
3	209392_at	ENPP2	-3.71	4.35E-10	4.24E-06	-0.62	-6.92	8q24.1
4	228011_at	LOC137392	-3.62	1.16E-09	4.40E-06	-0.61	-6.73	8q21.3
5	204044_at	QPRT	-2.52	1.20E-09	4.40E-06	-0.58	-6.65	16p12.1
6	204120_s_at	ADK	-1.62	6.49E-10	4.40E-06	-0.55	-6.64	10cen-q24
7	214698_at	ROD1	-1.66	1.03E-09	4.40E-06	-0.54	-6.54	9q32
8	226196_s_at	MGC16028	-2.18	1.11E-09	4.40E-06	-0.55	-6.54	14q24.2
9	203897_at	LOC57149	-1.68	2.94E-09	9.54E-06	-0.54	-6.40	16p11.2
10	206574_s_at	PTP4A3	-3.74	8.52E-09	1.46E-05	-0.58	-6.31	
11	210839_s_at	ENPP2	-2.27	7.95E-09	1.46E-05	-0.56	-6.30	8q24.1
12	227461_at	STN2	-2.75	6.51E-09	1.46E-05	-0.54	-6.28	14q31.1

13	215288_at	TRPC2	-2.77	6.53E-09	1.46E-05	-0.54	-6.26	11p15.4-p15.3
14	203050_at	TP53BP1	-1.50	5.11E-09	1.46E-05	-0.52	-6.24	15q15-q21
15	201427_s_at	SEPP1	-2.32	6.34E-09	1.46E-05	-0.52	-6.21	5q31
16	213800_at	HF1	-3.36	1.11E-08	1.62E-05	-0.54	-6.19	1q32
17	203373_at	SOCS2	-3.55	7.08E-09	1.46E-05	-0.52	-6.18	12q
18	202862_at	FAH	-1.89	9.54E-09	1.55E-05	-0.52	-6.16	15q23-q25
19	229971_at	GPR114	-2.06	8.07E-09	1.46E-05	-0.51	-6.13	16q12.2
20	225029_at		-1.52	1.05E-08	1.62E-05	-0.51	-6.08	
21	218188_s_at	TIMM13	-1.56	1.25E-08	1.66E-05	-0.50	-6.05	19p13.3
22	203581_at	RAB4A	-1.43	1.24E-08	1.66E-05	-0.50	-6.04	1q42-q43
23	221509_at	DENR	-1.42	1.88E-08	2.39E-05	-0.50	-5.96	12q24.31
24	214039_s_at	LAPTM4B	-2.80	2.73E-08	3.33E-05	-0.51	-5.96	8q22.1
25	228077_at		-1.51	2.95E-08	3.45E-05	-0.49	-5.87	
26	211727_s_at	COX11	-1.49	3.24E-08	3.61E-05	-0.49	-5.87	17q22
27	225237_s_at		-1.88	3.34E-08	3.61E-05	-0.49	-5.86	
28	204485_s_at	TOM1L1	-2.18	8.59E-08	8.97E-05	-0.49	-5.71	17q23.2
29	227860_at	CPXM	-2.14	1.11E-07	1.04E-04	-0.47	-5.62	20p12.3-p13
30	212640_at	LOC201562	-1.47	9.74E-08	9.82E-05	-0.47	-5.62	3q21.1
31	214697_s_at	ROD1	-1.48	1.02E-07	9.92E-05	-0.47	-5.61	9q32
32	243579_at	MSI2	-2.19	1.14E-07	1.04E-04	-0.47	-5.61	17q23.1
33	212070_at	GPR56	-3.01	1.81E-07	1.36E-04	-0.49	-5.59	16q13
34	214106_s_at	GMDS	-1.86	1.35E-07	1.16E-04	-0.47	-5.57	6p25
35	212364_at	MYO1B	-2.62	1.78E-07	1.36E-04	-0.48	-5.56	2q12-q34
36	224587_at	PC4	-1.40	1.35E-07	1.16E-04	-0.46	-5.55	5p13.3
37	202501_at	MAPRE2	-1.51	1.43E-07	1.19E-04	-0.46	-5.54	18q12.1
38	243526_at		-4.66	3.52E-07	2.19E-04	-0.53	-5.51	
39	220643_s_at	FAIM	-1.76	1.64E-07	1.33E-04	-0.46	-5.51	3q22.3
40	225240_s_at		-1.92	1.75E-07	1.36E-04	-0.46	-5.50	
41	74694_s_at	FRA	-1.42	1.96E-07	1.43E-04	-0.46	-5.47	16p12.1
42	225532_at	LOC91768	-1.83	2.20E-07	1.53E-04	-0.46	-5.46	18q11.1
43	230873_at	DKFZP434B103	-1.38	2.06E-07	1.47E-04	-0.45	-5.46	3p25.3
44	218395_at	FLJ13433	-1.48	2.33E-07	1.59E-04	-0.45	-5.44	12q23.2
45	229620_at	SEPP1	-2.57	3.63E-07	2.21E-04	-0.47	-5.41	5q31
46	234423_x_at		-1.62	3.11E-07	2.02E-04	-0.45	-5.40	
47	208767_s_at	LAPTM4B	-2.77	5.43E-07	2.78E-04	-0.50	-5.38	8q22.1
48	202043_s_at	SMS	-1.37	3.07E-07	2.02E-04	-0.45	-5.38	Xp22.1
49	223075_s_at	IBA2	-2.65	5.24E-07	2.78E-04	-0.48	-5.37	9q34.13-q34.3
50	242414_at		-2.00	3.82E-07	2.28E-04	-0.46	-5.36	

Table 2**2. All-Pairs (AP)****2.1 D835 versus Double**

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	219938_s_at	PSTPIP2	-2.38	1.83E-06	2.05E-02	-3.11	-10.48	18q12
2	209981_at	PIPPIN	-3.52	7.22E-04	3.56E-01	-3.27	-10.27	22q13.2-q13.31
3	201382_at	SIP	-2.36	1.12E-06	2.05E-02	-2.69	-9.65	1q24-q25
4	229395_at	STX4A	-1.24	3.24E-06	2.71E-02	-2.61	-9.39	16p11.2
5	222779_s_at	HSA277841	-1.89	1.58E-06	2.05E-02	-2.58	-9.29	17p13.3
6	210571_s_at	CMAH	-3.04	9.39E-04	3.65E-01	-2.68	-8.61	6p21.32
7	222583_s_at	NUP50	-2.04	1.31E-05	7.30E-02	-2.34	-8.07	22q13.31
8	238099_at	HSPA4	-2.98	8.49E-05	2.22E-01	-2.30	-8.04	5q31.1-q31.2
9	207764_s_at	HIPK3	-1.90	1.93E-05	9.25E-02	-2.27	-7.77	11p13
10	203138_at	HAT1	-1.96	2.41E-05	9.78E-02	-2.13	-7.63	2q31.2-q33.1
11	223148_at	PIGS	-1.51	1.27E-05	7.30E-02	-2.07	-7.47	17p13.2
12	221728_x_at		-5.56	1.34E-04	2.22E-01	-2.08	-7.29	
13	206544_x_at	SMARCA2	-2.35	2.63E-05	9.78E-02	-1.92	-6.90	9p22.3
14	204332_s_at	AGA	-2.17	3.07E-04	3.07E-01	-1.99	-6.88	4q32-q33
15	213983_s_at	KIAA0648	-1.82	4.10E-04	3.15E-01	-1.96	-6.75	4p14
16	222466_s_at	MRPL42	-1.99	1.05E-04	2.22E-01	-1.89	-6.72	12q22
17	243225_at		5.90	2.26E-04	2.75E-01	1.90	6.65	
18	217847_s_at	TRAP150	-1.82	1.97E-04	2.75E-01	-1.85	-6.53	1p34.3
19	205588_s_at	FOP	-1.81	6.35E-05	2.13E-01	-1.81	-6.40	6q27
20	215424_s_at	SNW1	-1.53	1.37E-04	2.22E-01	-1.90	-6.28	14q24.3
21	211762_s_at	KPNA2	-1.49	1.40E-04	2.22E-01	-1.72	-6.15	17q23.1-q23.3
22	212742_at	ZNF364	-1.71	9.48E-04	3.65E-01	-1.79	-6.13	1q21.1
23	241304_at	PIK3C3	4.03	1.35E-04	2.22E-01	1.70	6.10	18q12.3
24	200595_s_at	EIF3S10	-1.69	1.46E-04	2.22E-01	-1.78	-6.07	10q26
25	217496_s_at	IDE	-1.77	4.97E-04	3.20E-01	-1.74	-6.07	10q23-q25
26	213827_at	SNX26	-2.08	8.44E-05	2.22E-01	-1.68	-6.04	19q13.12
27	241114_s_at		-3.21	4.89E-03	4.30E-01	-1.92	-6.02	
28	243852_at	CGI-59	-1.97	3.00E-03	4.14E-01	-1.85	-6.01	7q34
29	219600_s_at	C21orf4	-1.79	9.44E-05	2.22E-01	-1.68	-6.00	21q22.11
30	218350_s_at	GMNN	-2.04	1.08E-04	2.22E-01	-1.64	-5.89	6p22.1
31	204082_at	PBX3	-2.08	2.09E-04	2.75E-01	-1.74	-5.87	9q33-q34
32	234204_at		5.84	1.13E-04	2.22E-01	1.62	5.84	
33	203772_at	BLVRA	-2.96	3.58E-04	3.07E-01	-1.64	-5.82	7p14-cen
34	224444_s_at	MGC14801	-2.51	1.81E-04	2.64E-01	-1.62	-5.81	1q32.2
35	201532_at	PSMA3	-1.79	2.21E-04	2.75E-01	-1.62	-5.79	14q23
36	221191_at	DKFZP434A0131	-1.69	1.29E-04	2.22E-01	-1.60	-5.75	7q11.23-q21.1
37	205899_at	CCNA1	-3.38	7.34E-03	4.49E-01	-1.85	-5.69	13q12.3-q13
38	209190_s_at	DIAPH1	-2.25	1.31E-03	4.02E-01	-1.66	-5.67	5q31
39	208905_at	CYCS	-1.83	4.38E-04	3.19E-01	-1.60	-5.65	7p15.2
40	229940_at	FLJ23027	-1.49	7.95E-04	3.57E-01	-1.61	-5.61	14q32.31
41	212438_at	RY1	-1.85	2.30E-04	2.75E-01	-1.58	-5.56	2p13.1
42	209739_s_at	DXS1283E	-5.90	2.50E-02	4.81E-01	-2.33	-5.54	Xp22.3

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43	210012_s_at	EWSR1	-3.37	2.35E-03	4.14E-01	-1.63	-5.48	22q12.2
44	202602_s_at	HTATSF1	-1.87	1.32E-03	4.02E-01	-1.57	-5.43	Xq26.1-q27.2
45	212863_x_at	CTBP1	-1.54	3.13E-04	3.07E-01	-1.51	-5.42	4p16
46	208308_s_at	GPI	-2.05	7.68E-04	3.57E-01	-1.53	-5.37	19q13.1
47	214218_s_at		-4.89	4.29E-03	4.28E-01	-1.63	-5.33	
48	203396_at	PSMA4	-1.81	2.55E-04	2.95E-01	-1.47	-5.29	15q24.1
49	235930_at		3.24	3.40E-04	3.07E-01	1.51	5.29	
50	227874_at		4.52	4.51E-04	3.20E-01	1.58	5.29	

2.2 D835 versus Status 1

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	207198_s_at	LIMS1	-1.91	8.16E-05	3.42E-01	-1.32	-5.69	2q12.2
2	211081_s_at	MAP4K5	-2.95	3.19E-05	3.42E-01	-1.14	-5.35	14q11.2-q21
3	238214_at		3.50	9.24E-05	3.42E-01	1.15	5.22	
4	212055_at	DKFZP586M1523	-2.30	2.99E-04	3.42E-01	-1.14	-4.86	18q12.1
5	223699_at	CPGL2	2.48	2.62E-04	3.42E-01	1.08	4.81	18q22.3
6	201606_s_at	PWP1	-2.17	1.48E-04	3.42E-01	-1.03	-4.76	12q24.11
7	223564_s_at	GNB1L	-2.32	1.33E-04	3.42E-01	-1.01	-4.72	22q11.2
8	240969_at		1.87	2.30E-04	3.42E-01	1.03	4.70	
9	225784_s_at	HCA127	-2.60	1.86E-04	3.42E-01	-1.01	-4.68	Xq11.1
10	231527_at		1.80	1.55E-04	3.42E-01	1.00	4.67	
11	210208_x_at	BAT3	-1.62	4.50E-04	3.42E-01	-1.06	-4.62	6p21.3
12	222573_s_at	SAV1	-2.46	3.35E-04	3.42E-01	-0.98	-4.50	14q13-q23
13	242563_at		2.60	3.41E-04	3.42E-01	0.98	4.49	
14	236187_s_at	MGC41939	2.19	4.58E-04	3.42E-01	0.96	4.39	6q21
15	244078_at		2.44	3.83E-04	3.42E-01	0.94	4.36	
16	228268_at	FMO2	1.83	1.04E-03	3.42E-01	1.04	4.34	1q23-q25
17	228278_at		-3.69	7.64E-04	3.42E-01	-1.01	-4.33	
18	205703_at	ATP6V0A2	2.77	1.03E-03	3.42E-01	1.03	4.32	12q24.31
19	229478_x_at	BIVM	-3.40	5.04E-04	3.42E-01	-0.94	-4.30	13q32-q33.1
20	214114_x_at	FASTK	-1.50	4.96E-04	3.42E-01	-0.94	-4.30	7q35
21	47571_at	ZNF236	1.88	8.03E-04	3.42E-01	0.97	4.27	18q22-q23
22	213872_at	FLJ12619	-1.75	4.75E-04	3.42E-01	-0.92	-4.25	6p22.1
23	221263_s_at	SF3b10	-1.72	7.90E-04	3.42E-01	-0.96	-4.24	6q24.1
24	216503_s_at		-2.04	4.97E-04	3.42E-01	-0.92	-4.24	
25	211228_s_at	RAD17	-1.52	4.55E-04	3.42E-01	-0.91	-4.24	5q13
26	229650_s_at	MGC2747	-1.70	5.58E-04	3.42E-01	-0.92	-4.21	19p13.11
27	237536_at		3.35	6.46E-04	3.42E-01	0.93	4.21	
28	203522_at	CCS	-3.32	7.50E-04	3.42E-01	-0.95	-4.21	11q13
29	223042_s_at	HCBP6	-1.73	4.80E-04	3.42E-01	-0.90	-4.21	Xq28
30	242052_at		1.82	7.87E-04	3.42E-01	0.94	4.20	
31	241891_at		2.03	8.32E-04	3.42E-01	0.93	4.18	
32	240785_at		1.86	5.73E-04	3.42E-01	0.90	4.17	
33	208756_at	EIF3S2	-1.34	5.73E-04	3.42E-01	-0.90	-4.16	1p34.1

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34	208879_x_at	C20orf14	-2.09	5.55E-04	3.42E-01	-0.87	-4.10	20q13.33
35	240493_at		1.92	1.56E-03	3.42E-01	0.98	4.10	
36	227553_at	P101-PI3K	2.90	1.46E-03	3.42E-01	0.95	4.07	17p13.1
37	234204_at		2.32	1.45E-03	3.42E-01	0.95	4.07	
38	201182_s_at	CHD4	-2.20	9.17E-04	3.42E-01	-0.89	-4.06	12p13
39	213961_s_at	TAF6L	1.69	8.16E-04	3.42E-01	0.88	4.05	11q12.2
40	234754_at		1.68	1.04E-03	3.42E-01	0.90	4.04	
41	230280_at	TRIM9	1.56	1.31E-03	3.42E-01	0.91	4.01	14q21.3
42	202143_s_at	COP9	-1.54	7.23E-04	3.42E-01	-0.85	-3.99	2q37.3
43	238589_s_at		1.78	8.08E-04	3.42E-01	0.86	3.98	
44	211630_s_at	GSS	-1.73	8.22E-04	3.42E-01	-0.85	-3.96	20q11.2
45	233043_at	LOC221814	2.26	1.97E-03	3.42E-01	0.94	3.95	7p21.2
46	222519_s_at	ESRRBL1	-1.75	1.32E-03	3.42E-01	-0.89	-3.94	3q13.12
47	231585_at	CHAC	2.32	1.75E-03	3.42E-01	0.90	3.91	9q21
48	243303_at		2.48	2.54E-03	3.42E-01	0.95	3.89	
49	222648_at	FLJ20748	2.56	1.96E-03	3.42E-01	0.90	3.88	17q25.3
50	237671_at		1.75	9.83E-04	3.42E-01	0.83	3.88	

2.3 D835 versus Status 2

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	208756_at	EIF3S2	-1.46	1.26E-07	4.14E-03	-1.37	-7.32	1p34.1
2	221664_s_at	F11R	-2.58	2.28E-06	3.74E-02	-1.13	-6.05	1q21.2- q21.3
3	229478_x_at	BIVM	-4.13	1.63E-05	1.38E-01	-1.00	-5.31	13q32- q33.1
4	243852_at	CGI-59	-2.42	3.29E-05	1.38E-01	-1.00	-5.18	7q34
5	205210_at	TGFBRAP1	-3.28	3.68E-05	1.38E-01	-0.95	-5.04	2q12.1
6	230528_s_at	MGC2752	-2.32	3.71E-05	1.38E-01	-0.94	-5.03	19p13.2
7	202427_s_at	DKFZP564B167	-1.65	3.09E-05	1.38E-01	-0.93	-5.00	1q24
8	223176_at	MGC14254	-2.78	3.35E-05	1.38E-01	-0.93	-4.99	6p21.2
9	200066_at - HG-U133B	IK	-1.49	3.97E-05	1.38E-01	-0.93	-4.96	5q31.3
10	208420_x_at	SUPT6H	-1.89	5.38E-05	1.60E-01	-0.94	-4.92	17q11.2
11	222451_s_at	ZDHHC9	-3.12	4.22E-05	1.38E-01	-0.91	-4.89	9
12	227669_at		-1.88	6.28E-05	1.67E-01	-0.92	-4.83	
13	227860_at	CPXM	-3.48	8.14E-05	1.67E-01	-0.90	-4.75	20p12.3- p13
14	212694_s_at	PCCB	-1.88	7.58E-05	1.67E-01	-0.88	-4.70	3q21-q22
15	239683_at	CLYBL	1.65	6.97E-05	1.67E-01	0.87	4.69	
16	221809_at	KIAA1464	-3.39	1.62E-04	1.77E-01	-0.96	-4.66	16q21
17	217785_s_at	YKT6	-2.30	1.00E-04	1.70E-01	-0.87	-4.65	7p15.1
18	201507_at	PFDN1	-1.50	7.92E-05	1.67E-01	-0.86	-4.65	5q31
19	219869_s_at	BIGM103	-1.70	1.27E-04	1.76E-01	-0.88	-4.64	4q22-q24
20	234766_at		2.20	3.21E-04	2.03E-01	0.93	4.59	
21	223364_s_at	DDX37	-3.17	9.42E-05	1.70E-01	-0.85	-4.59	12q24.31
22	218367_x_at	USP21	-2.12	9.65E-05	1.70E-01	-0.85	-4.58	1q22
23	211503_s_at	RAB14	-1.65	1.04E-04	1.70E-01	-0.85	-4.57	9q32- q34.11

24	203597_s_at	WBP4	-1.67	1.40E-04	1.76E-01	-0.86	-4.56	13q13.3
25	219141_s_at	FLJ20294	-2.33	1.22E-04	1.76E-01	-0.84	-4.51	11p11.12
26	224821_at	MGC15429	-1.90	1.35E-04	1.76E-01	-0.84	-4.48	3p21.31
27	202122_s_at	TIP47	-1.53	1.26E-04	1.76E-01	-0.83	-4.47	19p13.3
28	213190_at	COG7	-3.02	1.35E-04	1.76E-01	-0.83	-4.45	16p12.3
29	212742_at	ZNF364	-1.65	1.46E-04	1.77E-01	-0.82	-4.42	1q21.1
30	209179_s_at	LENG4	-2.04	1.56E-04	1.77E-01	-0.82	-4.41	19q13.4
31	235040_at	DKFZp761H0421	-2.95	3.06E-04	2.03E-01	-0.91	-4.40	17q21.2
32	207223_s_at	ROD1	-1.39	2.33E-04	2.03E-01	-0.85	-4.39	9q32
33	228495_at		-1.76	1.61E-04	1.77E-01	-0.81	-4.38	
34	224914_s_at	CIP29	-1.65	2.64E-04	2.03E-01	-0.83	-4.35	12q13.13
35	241813_at	MBD1	-2.62	5.08E-04	2.17E-01	-0.87	-4.34	18q21
36	202593_s_at	MIR16	-1.78	1.88E-04	1.96E-01	-0.81	-4.34	16p12-p11.2
37	201175_at	CGI-31	-1.70	1.91E-04	1.96E-01	-0.81	-4.33	11cen-q22.3
38	215710_at	SIAT4C	-3.32	3.55E-04	2.03E-01	-0.89	-4.33	11q23-q24
39	208962_s_at	FADS1	-3.74	2.81E-04	2.03E-01	-0.84	-4.32	11q12.2-q13.1
40	224068_x_at	FLJ10290	-1.54	2.00E-04	1.99E-01	-0.80	-4.30	5q33.1
41	224913_s_at	TIM50L	-2.52	2.19E-04	2.03E-01	-0.80	-4.28	19q13.13
42	221499_s_at	NPEPL1	-1.58	2.17E-04	2.03E-01	-0.79	-4.27	20q13.32
43	201284_s_at	APEH	-2.30	2.60E-04	2.03E-01	-0.80	-4.25	3p21.31
44	201932_at	MUF1	-2.44	2.58E-04	2.03E-01	-0.80	-4.25	1p33
45	220996_s_at	C1orf14	2.90	8.82E-04	2.45E-01	0.89	4.25	1q25
46	239860_at		1.72	1.26E-03	2.64E-01	0.94	4.23	
47	222527_s_at	FLJ10290	-1.76	2.56E-04	2.03E-01	-0.78	-4.21	5q33.1
48	225937_at		-2.63	2.58E-04	2.03E-01	-0.78	-4.21	
49	228444_at	ARRB1	-2.81	3.44E-04	2.03E-01	-0.79	-4.19	11q13
50	226445_s_at	TRIM41	-1.47	3.52E-04	2.03E-01	-0.80	-4.19	5q35.3

2.4 D835 versus Status 3

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	209179_s_at	LENG4	-2.52	3.15E-08	6.93E-04	-1.12	-7.01	19q13.4
2	205227_at	IL1RAP	-3.99	2.23E-07	2.46E-03	-1.03	-6.38	3q28
3	213800_at	HF1	-7.26	1.29E-06	5.40E-03	-1.00	-5.99	1q32
4	208962_s_at	FADS1	-3.60	7.59E-07	5.40E-03	-0.95	-5.94	11q12.2-q13.1
5	223364_s_at	DDX37	-3.78	9.89E-07	5.40E-03	-0.94	-5.87	12q24.31
6	201242_s_at	ATP1B1	-2.95	1.52E-06	5.40E-03	-0.92	-5.72	1q22-q25
7	233013_x_at		-1.54	1.96E-06	5.40E-03	-0.92	-5.68	
8	238959_at	LOC113251	-2.66	1.86E-06	5.40E-03	-0.91	-5.65	12q13.12
9	235852_at		-6.81	3.55E-06	7.40E-03	-0.94	-5.63	
10	209899_s_at	SIAHBP1	-1.52	1.14E-05	8.73E-03	-0.96	-5.62	8q24.2-qtel
11	209392_at	ENPP2	-5.76	4.03E-06	7.40E-03	-0.95	-5.61	8q24.1
12	208996_s_at	POLR2C	-1.52	3.99E-06	7.40E-03	-0.90	-5.56	16q13-q21
13	211182_x_at		-3.75	2.72E-06	6.65E-03	-0.89	-5.53	

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14	225233_at		-5.57	7.66E-06	8.23E-03	-0.92	-5.40	
15	206574_s_at	PTP4A3	-5.41	4.95E-06	8.23E-03	-0.88	-5.40	
16	200820_at	PSMD8	-1.71	6.01E-06	8.23E-03	-0.86	-5.34	19q13.13
17	220974_x_at	BA108L7.2	-2.32	5.41E-06	8.23E-03	-0.86	-5.34	10q24.31
18	201932_at	MUF1	-2.30	6.83E-06	8.23E-03	-0.86	-5.33	1p33
19	240969_at		2.04	6.94E-05	1.52E-02	0.97	5.31	
20	236269_at	LOC89887	-1.73	5.77E-06	8.23E-03	-0.85	-5.29	19
21	219254_at	FLJ22222	-4.20	8.42E-06	8.23E-03	-0.87	-5.27	17q25.3
22	217226_s_at	BA108L7.2	-2.13	6.51E-06	8.23E-03	-0.85	-5.27	10q24.31
23	214697_s_at	ROD1	-1.98	3.95E-05	1.23E-02	-0.91	-5.25	9q32
24	208791_at	CLU	-11.11	1.29E-05	8.73E-03	-0.90	-5.24	8p21-p12
25	218118_s_at	TIMM23	-1.64	1.21E-05	8.73E-03	-0.85	-5.20	10q11.21-q11.23
26	200619_at	SF3B2	-1.83	2.57E-05	1.08E-02	-0.88	-5.20	11q13.1
27	201243_s_at	ATP1B1	-2.55	8.08E-06	8.23E-03	-0.83	-5.20	1q22-q25
28	212742_at	ZNF364	-1.53	3.12E-05	1.18E-02	-0.88	-5.20	1q21.1
29	200721_s_at	ACTR1A	-1.68	7.85E-06	8.23E-03	-0.83	-5.20	10q24.32
30	221664_s_at	F11R	-2.29	1.66E-05	8.74E-03	-0.86	-5.19	1q21.2-q21.3
31	221754_s_at	CORO1B	-4.24	2.64E-05	1.08E-02	-0.87	-5.17	11q13.1
32	237524_at		2.47	4.29E-04	3.21E-02	1.21	5.17	
33	201723_s_at	GALNT1	-1.45	5.21E-05	1.37E-02	-0.90	-5.16	18q12.1
34	225257_at	MGC20255	-1.79	3.59E-05	1.23E-02	-0.88	-5.16	19q13.13
35	221809_at	KIAA1464	-2.79	1.21E-05	8.73E-03	-0.85	-5.16	16q21
36	212968_at	RFNG	-1.57	8.93E-06	8.23E-03	-0.83	-5.16	17q25
37	202111_at	SLC4A2	-5.58	1.57E-05	8.74E-03	-0.88	-5.16	7q35-q36
38	243579_at	MSI2	-3.43	8.96E-06	8.23E-03	-0.82	-5.15	17q23.1
39	217849_s_at	CDC42BPB	-4.41	1.49E-05	8.74E-03	-0.83	-5.12	14q32.3
40	211501_s_at	EIF3S9	-1.84	1.11E-05	8.73E-03	-0.83	-5.12	7p22.3
41	228678_at		-4.01	1.14E-05	8.73E-03	-0.83	-5.12	
42	230482_at		2.49	1.64E-04	2.05E-02	0.98	5.11	
43	208761_s_at	UBL1	-1.45	1.31E-05	8.73E-03	-0.83	-5.11	2q33
44	209739_s_at	DXS1283E	-3.12	1.07E-05	8.73E-03	-0.82	-5.09	Xp22.3
45	238589_s_at		1.62	7.91E-05	1.61E-02	0.90	5.08	
46	221499_s_at	NPEPL1	-1.73	1.31E-05	8.73E-03	-0.81	-5.04	20q13.32
47	208756_at	EIF3S2	-1.36	1.53E-05	8.74E-03	-0.81	-5.04	1p34.1
48	201526_at	ARF5	-1.71	1.37E-05	8.74E-03	-0.80	-5.01	7q31.3
49	207223_s_at	ROD1	-1.37	1.52E-05	8.74E-03	-0.81	-5.01	9q32
50	223176_at	MGC14254	-2.55	1.61E-05	8.74E-03	-0.80	-4.99	6p21.2

2.5 D835 versus Status 4

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	201242_s_at	ATP1B1	-4.39	1.51E-08	3.57E-04	-3.73	-14.27	1q22-q25
2	218983_at	LOC51279	-3.66	7.69E-05	8.25E-02	-2.73	-9.33	12p13.31
3	221942_s_at	GUCY1A3	-5.20	5.27E-05	7.94E-02	-2.63	-9.19	4q31.1-q31.2
4	201005_at	CD9	-10.35	4.65E-04	1.27E-01	-3.10	-9.07	12p13.3

5	210425_x_at	GOLGIN-67	-3.52	5.58E-05	7.94E-02	-2.40	-8.54 15q11.2
6	220974_x_at	BA108L7.2	-4.34	3.14E-04	1.24E-01	-2.63	-8.46 10q24.31
7	201243_s_at	ATP1B1	-3.98	1.93E-04	1.06E-01	-2.34	-7.99 1q22-q25
8	230589_at		-3.36	1.13E-05	6.65E-02	-1.97	-7.53
9	205081_at	CRIP1	-3.83	3.07E-05	7.28E-02	-2.00	-7.48 7q11.23
10	222138_s_at	WDR13	-3.08	7.46E-05	8.25E-02	-2.03	-7.40 Xp11.23
11	217226_s_at	BA108L7.2	-3.56	1.07E-03	1.36E-01	-2.46	-7.32 10q24.31
12	226959_at		-5.23	6.01E-04	1.27E-01	-2.26	-7.32
13	201069_at	MMP2	-5.72	2.24E-04	1.06E-01	-2.10	-7.32 16q13-q21
14	202111_at	SLC4A2	-14.46	1.90E-03	1.44E-01	-2.90	-7.18 7q35-q36
15	235391_at	LOC137392	-3.80	6.39E-05	7.94E-02	-1.94	-7.16 8q21.3
16	204073_s_at	C11orf9	-3.61	2.14E-04	1.06E-01	-2.03	-7.13 11q12-q13.1
17	213983_s_at	KIAA0648	-1.87	2.28E-05	7.28E-02	-1.87	-7.10 4p14
18	204341_at	TRIM16	-2.78	4.14E-04	1.27E-01	-2.09	-7.09 17p11.2
19	206574_s_at	PTP4A3	-13.49	1.75E-03	1.43E-01	-2.58	-7.03
20	212221_x_at		-3.00	1.65E-04	1.06E-01	-1.95	-7.00
21	225178_at	FLJ00166	-2.29	9.70E-06	6.65E-02	-1.81	-6.99 3q27.2
22	45297_at	MGC45806	-5.50	7.13E-04	1.30E-01	-2.14	-6.98 1p35.2
23	212608_s_at		-2.06	1.10E-05	6.65E-02	-1.78	-6.90
24	39248_at	AQP3	-6.18	8.49E-04	1.32E-01	-2.06	-6.71 9p13
25	211727_s_at	COX11	-2.51	2.50E-05	7.28E-02	-1.72	-6.62 17q22
26	203897_at	LOC57149	-2.79	4.02E-04	1.27E-01	-1.88	-6.58 16p11.2
27	212605_s_at		-3.17	1.96E-04	1.06E-01	-1.81	-6.56
28	224901_at		-3.91	1.62E-03	1.43E-01	-2.15	-6.51
29	219251_s_at	FLJ10300	-2.82	2.75E-05	7.28E-02	-1.69	-6.46 7q36.3
30	230864_at	MGC42105	3.15	5.41E-05	7.94E-02	1.72	6.38 5p11
31	227227_at		-1.99	3.39E-05	7.28E-02	-1.64	-6.34
32	216842_x_at		2.25	3.28E-05	7.28E-02	1.62	6.27
33	219964_at	ST7L	-2.47	3.23E-05	7.28E-02	-1.61	-6.23 1p13.1
34	202371_at	FLJ21174	-2.33	6.28E-05	7.94E-02	-1.66	-6.21 Xq22.1
35	202438_x_at		-2.29	7.15E-05	8.25E-02	-1.62	-6.19
36	209695_at	PTP4A3	-2.61	1.70E-03	1.43E-01	-1.96	-6.15
37	243526_at		-18.10	3.64E-03	1.51E-01	-2.54	-6.08
38	201613_s_at	RUVBL1	-2.47	3.39E-04	1.27E-01	-1.68	-6.07 3q21
39	224093_at	IFNK	13.22	1.75E-04	1.06E-01	1.80	6.06
40	204247_s_at	CDK5	-2.75	5.88E-05	7.94E-02	-1.59	-6.05 7q36
41	202247_s_at	MTA1	-1.61	2.23E-04	1.06E-01	-1.62	-6.01 14q32.3
42	225010_at	D10S170	-2.51	4.93E-05	7.94E-02	-1.55	-5.98 10q21
43	208978_at	CRIP2	-16.29	3.53E-03	1.51E-01	-2.28	-5.98 14q32.3
44	227431_at		-2.35	1.15E-03	1.37E-01	-1.76	-5.91
45	201307_at	FLJ10849	-2.93	1.02E-03	1.36E-01	-1.71	-5.86 4q21.21
46	242313_at		-2.17	2.54E-04	1.11E-01	-1.58	-5.86
47	222244_s_at	FLJ20618	-1.75	6.35E-05	7.94E-02	-1.52	-5.86 22q12.2
48	233935_at		4.08	1.20E-04	8.56E-02	1.53	5.75
49	210123_s_at	CHRNA7	-2.43	1.81E-04	1.06E-01	-1.52	-5.73 15q14
50	220938_s_at	GMEB1	-2.96	2.70E-04	1.12E-01	-1.54	-5.72 1p35.2

2.6 D835 versus Status 5

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	215732_s_at	DTX2	2.65	2.86E-05	2.38E-01	1.56	6.18	7q11.23
2	201523_x_at	UBE2N	-1.49	5.01E-05	2.38E-01	-1.48	-5.90	12q22
3	209531_at	GSTZ1	-3.54	7.08E-05	2.38E-01	-1.49	-5.87	14q24.3
4	219869_s_at	BIGM103	-2.03	9.47E-05	2.38E-01	-1.50	-5.85	4q22-q24
5	218489_s_at	ALAD	-2.44	5.43E-04	2.38E-01	-1.48	-5.47	9q34
6	229976_at		3.20	1.51E-04	2.38E-01	1.38	5.44	
7	221370_at	ZNF73	3.82	1.63E-04	2.38E-01	1.39	5.38	22p
8	208007_at		5.50	4.11E-04	2.38E-01	1.48	5.27	
9	240935_at		2.91	3.31E-04	2.38E-01	1.38	5.18	
10	47571_at	ZNF236	2.12	3.15E-04	2.38E-01	1.33	5.10	18q22-q23
11	207842_s_at	MLN51	-1.62	1.83E-04	2.38E-01	-1.28	-5.10	17q11-q21.3
12	233752_s_at	ATBF1	1.48	2.00E-04	2.38E-01	1.28	5.08	16q22.3-q23.1
13	220996_s_at	C1orf14	4.04	3.21E-04	2.38E-01	1.32	5.06	1q25
14	243579_at	MSI2	-3.64	1.19E-03	2.38E-01	-1.37	-4.97	17q23.1
15	235838_at		1.89	2.79E-04	2.38E-01	1.25	4.95	
16	214324_at	GP2	3.16	2.81E-04	2.38E-01	1.26	4.94	9q21.11-q21.2
17	232184_at	ALS2	-2.15	5.41E-04	2.38E-01	-1.27	-4.92	2q33.2
18	227431_at		-2.01	1.22E-03	2.38E-01	-1.34	-4.90	
19	224218_s_at	TRPS1	3.85	5.82E-04	2.38E-01	1.32	4.88	8q24.12
20	222451_s_at	ZDHHC9	-3.05	4.38E-04	2.38E-01	-1.24	-4.87	9
21	240016_at		3.37	5.17E-04	2.38E-01	1.27	4.82	
22	214408_s_at	RFPL3S	2.55	4.74E-04	2.38E-01	1.22	4.75	22q12.3
23	243893_at		3.39	3.36E-04	2.38E-01	1.18	4.71	
24	208573_s_at	OR2H3	2.43	4.02E-04	2.38E-01	1.19	4.70	6p21.3
25	205353_s_at	PBP	-1.99	3.82E-04	2.38E-01	-1.17	-4.69	12q24.23
26	200820_at	PSMD8	-1.93	2.28E-03	2.38E-01	-1.33	-4.68	19q13.13
27	229352_at	MGC24663	7.93	8.87E-04	2.38E-01	1.29	4.68	15q22.31
28	201329_s_at	ETS2	-1.67	1.09E-03	2.38E-01	-1.23	-4.67	21q22.2
29	221535_at	FLJ11301	-1.80	6.71E-04	2.38E-01	-1.18	-4.61	3q29
30	213244_at	SCAMP-4	-2.28	1.83E-03	2.38E-01	-1.27	-4.61	19p13.3
31	240910_at		2.77	4.25E-04	2.38E-01	1.15	4.60	
32	219791_s_at	FLJ11539	2.80	7.79E-04	2.38E-01	1.21	4.58	4q34.1
33	236676_at		2.57	6.73E-04	2.38E-01	1.18	4.57	
34	237503_at	AIT	2.86	9.87E-04	2.38E-01	1.24	4.57	12q23.3
35	215537_x_at	DDAH2	-1.75	1.11E-03	2.38E-01	-1.28	-4.57	6p21.3
36	206301_at	TEC	-4.70	5.23E-03	2.38E-01	-1.53	-4.55	4p12
37	244540_at		5.21	1.17E-03	2.38E-01	1.27	4.54	
38	201524_x_at	UBE2N	-1.51	4.64E-04	2.38E-01	-1.14	-4.54	12q22
39	220851_at	PRO1600	3.24	5.54E-04	2.38E-01	1.15	4.53	9p24.2
40	234431_at		2.07	4.95E-04	2.38E-01	1.14	4.53	
41	225233_at		-3.67	4.59E-03	2.38E-01	-1.42	-4.51	
42	202799_at	CLPP	-1.59	5.43E-04	2.38E-01	-1.12	-4.46	19p13.3

51

43 220011_at	MGC2603	1.52	5.47E-04	2.38E-01	1.11	4.45 1p35.3
44 219766_at	MGC4093	-2.96	7.46E-04	2.38E-01	-1.13	-4.45 19q13.13
45 201757_at	NDUFS5	-1.76	6.05E-04	2.38E-01	-1.11	-4.45 1p34.2-p33
46 216921_s_at	KRTHA5	3.05	6.28E-04	2.38E-01	1.12	4.44 17q12-q21
47 228421_s_at	EFEMP1	4.50	6.32E-04	2.38E-01	1.12	4.44 2p16
48 243010_at	MSI2	-2.01	8.74E-04	2.38E-01	-1.15	-4.43 17q23.1
49 237411_at	LOC153516	3.77	5.95E-04	2.38E-01	1.11	4.43 5q12.2
50 205247_at	NOTCH4	1.89	6.25E-04	2.38E-01	1.11	4.42 6p21.3

2.7 D835 versus normal

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	235040_at	DKFZp761H0421	-2.50	9.69E-09	3.57E-04	-0.78	-6.53	17q21.2
2	222425_s_at	DKFZP586F1524	-2.50	4.05E-06	1.24E-02	-0.71	-5.53	17q11.1
3	200721_s_at	ACTR1A	-1.48	3.45E-06	1.18E-02	-0.69	-5.48	10q24.32
4	221809_at	KIAA1464	-3.80	8.68E-07	9.88E-03	-0.66	-5.45	16q21
5	236140_at	GCLM	-3.83	9.20E-07	9.88E-03	-0.65	-5.42	1p22.1
6	208420_x_at	SUPT6H	-1.79	1.29E-06	9.88E-03	-0.64	-5.35	17q11.2
7	202974_at	MPP1	-1.75	1.34E-06	9.88E-03	-0.63	-5.31	Xq28
8	219254_at	FLJ22222	-3.00	1.66E-06	1.01E-02	-0.63	-5.28	17q25.3
9	208996_s_at	POLR2C	-1.39	3.95E-05	2.79E-02	-0.74	-5.25	16q13-q21
10	211003_x_at	TGM2	-6.34	2.38E-06	1.01E-02	-0.64	-5.20	20q12
11	210248_at	WNT7A	-2.55	2.17E-06	1.01E-02	-0.62	-5.20	3p25
12	213714_at	CACNB2	-3.28	2.48E-06	1.01E-02	-0.61	-5.14	10p12
13	224947_at	RNF26	-1.51	4.62E-05	2.94E-02	-0.71	-5.13	11q23
14	225099_at	LOC200933	-1.85	9.76E-06	2.00E-02	-0.63	-5.07	3q29
15	210639_s_at	APG5L	-1.38	1.80E-05	2.30E-02	-0.65	-5.06	6q21
16	210036_s_at	KCNH2	-2.85	3.52E-06	1.18E-02	-0.60	-5.05	7q35-q36
17	211228_s_at	RAD17	-1.45	4.46E-05	2.94E-02	-0.68	-5.02	5q13
18	227669_at		-1.55	1.68E-05	2.30E-02	-0.64	-5.01	
19	202593_s_at	MIR16	-1.85	5.95E-06	1.45E-02	-0.61	-5.01	16p12-p11.2
20	210571_s_at	CMAH	-1.99	1.44E-05	2.30E-02	-0.63	-5.01	6p21.32
21	237403_at	GF11B	-4.81	5.06E-06	1.41E-02	-0.60	-4.97	9q34.13
22	200070_at - HG-U133B	CGI-57	-1.57	1.60E-05	2.30E-02	-0.63	-4.97	2q35
23	202427_s_at	DKFZP564B167	-1.47	2.96E-05	2.56E-02	-0.65	-4.96	1q24
24	215054_at	EPOR	-2.81	5.37E-06	1.41E-02	-0.59	-4.95	19p13.3-p13.2
25	205262_at	KCNH2	-4.98	6.31E-06	1.45E-02	-0.58	-4.89	7q35-q36
26	200066_at - HG-U133B	IK	-1.39	1.03E-04	3.93E-02	-0.69	-4.89	5q31.3
27	212100_s_at	KIAA1649	-1.25	1.82E-05	2.30E-02	-0.60	-4.82	22q13.2
28	223818_s_at	HBXAP	-2.73	2.04E-05	2.30E-02	-0.60	-4.80	11q13.3
29	231724_at	CRSP7	-2.81	9.19E-06	1.99E-02	-0.57	-4.80	19p13.11
30	222527_s_at	FLJ10290	-1.64	6.37E-05	3.30E-02	-0.64	-4.79	5q33.1
31	212598_at	ALFY	-2.62	2.52E-05	2.56E-02	-0.60	-4.76	4q21.3
32	215654_at	BCAT2	-2.21	2.18E-05	2.30E-02	-0.59	-4.76	19q13

33 223176_at	MGC14254	-2.07	9.74E-05	3.93E-02	-0.65	-4.73 6p21.2
34 211598_x_at		-2.99	1.63E-04	4.71E-02	-0.68	-4.72
35 230285_at	DKFZp313A2432	-1.73	2.17E-05	2.30E-02	-0.58	-4.72 11p14.2
36 221499_s_at	NPEPL1	-1.49	8.40E-05	3.73E-02	-0.63	-4.70 20q13.32
37 241813_at	MBD1	-2.79	1.69E-04	4.83E-02	-0.67	-4.70 18q21
38 237215_s_at		-3.23	2.75E-05	2.56E-02	-0.58	-4.70
39 214446_at	ELL2	-3.99	1.38E-05	2.30E-02	-0.56	-4.70 5q14.3
40 225235_at	MGC14859	-2.18	1.35E-05	2.30E-02	-0.56	-4.69 5q35.3
41 209764_at		-2.87	1.45E-05	2.30E-02	-0.56	-4.67
42 212065_s_at	KIAA0570	-1.92	7.96E-05	3.58E-02	-0.62	-4.67 2p14
43 209179_s_at	LENG4	-1.73	1.07E-04	3.93E-02	-0.63	-4.67 19q13.4
44 202111_at	SLC4A2	-2.97	1.55E-05	2.30E-02	-0.55	-4.65 7q35-q36
45 205592_at	SLC4A1	-3.79	1.58E-05	2.30E-02	-0.55	-4.64 17q21-q22
46 202815_s_at	HIS1	-1.55	6.34E-05	3.30E-02	-0.60	-4.64 17q21.32
47 208916_at	SLC1A5	-2.07	2.02E-05	2.30E-02	-0.55	-4.62 19q13.3
48 236981_at		-6.30	2.13E-05	2.30E-02	-0.58	-4.61
49 202151_s_at	GDBR1	-2.24	3.26E-05	2.56E-02	-0.56	-4.60 9q34.3
50 208501_at	GFI1B	-2.98	2.71E-05	2.56E-02	-0.56	-4.60 9q34.13

2.8 Double versus Status 1

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	240676_at		3.54	6.52E-09	2.46E-04	3.50	13.57	
2	222583_s_at	NUP50	2.48	5.24E-08	9.89E-04	3.09	11.70	22q13.31
3	210820_x_at	COQ7	1.61	2.08E-07	2.62E-03	2.70	10.44	16p13.11- p12.3
4	205282_at	LRP8	2.12	5.17E-07	4.88E-03	2.49	9.46	1p34
5	223564_s_at	GNB1L	-5.22	8.27E-07	6.24E-03	-2.39	-9.07	22q11.2
6	220623_s_at	TSGA10	2.45	1.42E-06	6.68E-03	2.36	8.84	2q11.2
7	215225_s_at	GPR17	2.56	9.92E-07	6.24E-03	2.29	8.77	2q21
8	202228_s_at	SDFR1	2.36	1.19E-06	6.41E-03	2.29	8.71	15q22
9	218728_s_at	HSPC163	2.05	2.86E-06	1.20E-02	2.26	8.39	1q42.12
10	218438_s_at	EG1	1.73	2.93E-04	1.11E-01	2.32	8.27	4p16
11	200595_s_at	EIF3S10	1.64	3.65E-06	1.38E-02	2.11	7.97	10q26
12	240354_at	MGC35033	1.99	8.25E-06	2.18E-02	2.19	7.78	12q13.11
13	227064_at		1.37	6.80E-06	2.14E-02	1.98	7.64	
14	205180_s_at	ADAM8	3.07	1.40E-04	7.93E-02	2.06	7.59	10q26.3
15	236898_at		4.98	1.24E-03	1.85E-01	2.22	7.58	
16	222779_s_at	HSA277841	1.72	4.46E-06	1.53E-02	1.94	7.51	17p13.3
17	221156_x_at	CPR8	2.01	2.67E-03	2.44E-01	2.27	7.41	15q21.1
18	208700_s_at	TKT	2.09	8.86E-06	2.18E-02	1.95	7.35	3p14.3
19	217246_s_at	EPAG	4.10	1.88E-03	2.15E-01	2.19	7.35	X
20	210118_s_at	IL1A	2.61	1.82E-04	8.92E-02	1.99	7.32	2q14
21	244257_at		2.37	1.29E-04	7.93E-02	1.97	7.30	
22	204633_s_at	RPS6KA5	2.42	1.43E-04	7.93E-02	1.96	7.27	14q31- q32.1
23	206841_at	PDE6H	5.51	1.07E-02	3.72E-01	2.63	7.17	12p13

24	213656_s_at		1.67	1.66E-03	2.05E-01	2.09	7.11
25	236001_at		1.54	9.05E-06	2.18E-02	1.83	7.09
26	208374_s_at	CAPZA1	1.68	9.22E-06	2.18E-02	1.84	7.07 1p13.1
27	219445_at	GLTSCR1	1.64	1.15E-05	2.18E-02	1.84	7.01 19q13.3
28	234372_at		2.02	8.49E-05	5.96E-02	1.85	6.96
29	218109_s_at	FLJ14153	1.76	1.39E-05	2.38E-02	1.84	6.96 3q25.32
30	234598_at		1.64	1.15E-05	2.18E-02	1.79	6.93
31	214037_s_at	JM1	1.79	1.53E-05	2.49E-02	1.84	6.93 Xp11.23
32	237092_at		1.80	1.05E-05	2.18E-02	1.79	6.93
33	236737_at	FLJ31528	2.85	2.67E-05	3.36E-02	1.94	6.86 17q25.3
34	203983_at	TSNAX	1.91	1.16E-05	2.18E-02	1.77	6.86 1q42.1
35	205446_s_at	ATF2	2.07	1.26E-05	2.27E-02	1.76	6.80 2q32
36	239342_at	DGKZ	1.70	8.69E-05	5.96E-02	1.79	6.75 11p11.2
37	45714_at	HPIP	1.41	1.69E-05	2.55E-02	1.74	6.72 16p13.3
38	222673_x_at	LOC159090	1.51	1.59E-05	2.49E-02	1.73	6.71 Xq26.3
39	220419_s_at	USP25	1.74	1.20E-03	1.81E-01	1.89	6.62 21q11.2
40	219802_at	FLJ22028	1.50	2.94E-05	3.36E-02	1.72	6.62 12p12.1
41	230724_s_at	FLJ10726	1.57	1.98E-05	2.82E-02	1.71	6.61 11q23.2
42	236396_at		3.02	1.28E-03	1.85E-01	1.88	6.59
43	214038_at	CCL8	2.40	2.02E-05	2.82E-02	1.72	6.58 17q11.2
44	204614_at	SERPINB2	13.04	2.08E-02	4.32E-01	3.05	6.55 18q21.3
45	221481_x_at	HNRPD	1.38	6.54E-05	5.44E-02	1.71	6.52 4q21.1-q21.2
46	209476_at	TXNDC	1.70	2.91E-05	3.36E-02	1.74	6.52 14q21.3
47	218861_at	RNF25	3.50	1.65E-02	4.12E-01	2.57	6.51 2q35
48	238099_at	HSPA4	2.69	6.37E-05	5.44E-02	1.70	6.50 5q31.1-q31.2
49	218538_s_at	MRS2L	1.73	2.09E-05	2.82E-02	1.67	6.47 6p22.3-p22.1
50	214396_s_at	MBD2	2.04	2.76E-05	3.36E-02	1.71	6.47 18q21

2.9 Double versus Status 2

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	226245_at		1.61	1.26E-07	5.22E-03	1.87	8.69	
2	221728_x_at		4.65	4.96E-04	1.65E-01	2.03	8.18	
3	237548_at		2.07	4.43E-04	1.55E-01	1.95	7.96	
4	213911_s_at	H2AFZ	1.39	9.73E-07	1.08E-02	1.69	7.81	4q24
5	220623_s_at	TSGA10	1.88	3.24E-07	5.22E-03	1.63	7.56	2q11.2
6	208700_s_at	TKT	1.71	3.52E-07	5.22E-03	1.60	7.45	3p14.3
7	203772_at	BLVRA	3.32	3.06E-04	1.27E-01	1.67	7.07	7p14-cen
8	204083_s_at	TPM2	-11.16	1.21E-06	1.08E-02	-1.51	-6.95	9p13.2-p13.1
9	241655_at		2.16	1.85E-06	1.17E-02	1.48	6.93	
10	214037_s_at	JM1	1.75	1.51E-06	1.12E-02	1.46	6.79	Xp11.23
11	213827_at	SNX26	1.83	1.28E-05	3.57E-02	1.48	6.77	19q13.12
12	201464_x_at	JUN	1.69	2.85E-06	1.59E-02	1.41	6.59	1p32-p31
13	36552_at	DKFZP586P0123	1.43	1.51E-03	2.42E-01	1.60	6.43	11q13.3

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14	210118_s_at	IL1A	2.48	9.02E-05	7.10E-02	1.44	6.43 2q14
15	219392_x_at	FLJ11029	1.71	3.68E-04	1.38E-01	1.50	6.43 17q23.2
16	214092_x_at	SFRS14	1.41	3.94E-06	1.60E-02	1.39	6.40 19p12
17	200595_s_at	EIF3S10	1.38	3.85E-06	1.60E-02	1.35	6.31 10q26
18	201382_at	SIP	1.78	3.78E-06	1.60E-02	1.34	6.30 1q24-q25
19	200030_s_at - HG-U133A	SLC25A3	-1.22	6.71E-05	7.10E-02	-1.39	-6.25 12q23
20	206841_at	PDE6H	3.84	9.83E-03	4.73E-01	1.87	6.24 12p13
21	239246_at		1.95	3.70E-05	6.60E-02	1.36	6.19
22	205962_at	PAK2	4.02	2.13E-02	6.01E-01	2.35	6.07 3q29
23	204332_s_at	AGA	1.83	7.64E-04	1.86E-01	1.42	6.01 4q32-q33
24	229697_at		1.51	2.44E-04	1.18E-01	1.37	6.01
25	215587_x_at		2.99	8.49E-03	4.52E-01	1.72	6.00
26	244125_at		-5.79	9.34E-06	3.46E-02	-1.30	-5.98
27	214630_at	CYP11B2	2.06	6.01E-04	1.73E-01	1.36	5.86 8q21-q22
28	208064_s_at	SIAT8C	-5.23	1.27E-05	3.57E-02	-1.26	-5.82 18q21.2
29	243613_at	MGC24039	1.77	1.22E-05	3.57E-02	1.24	5.78 12p11.21
30	242573_at		1.79	2.34E-04	1.16E-01	1.30	5.77
31	241536_at		1.84	1.21E-05	3.57E-02	1.23	5.77
32	211987_at	TOP2B	1.57	1.74E-03	2.62E-01	1.40	5.76 3p24
33	234809_at	HCA127	3.71	1.41E-02	5.27E-01	1.78	5.75 Xq11.1
34	AFFX-BioDn-5_at - HG-U133A		1.35	7.88E-04	1.86E-01	1.34	5.72
35	208891_at	DUSP6	1.96	3.58E-05	6.60E-02	1.23	5.72 12q22-q23
36	232322_x_at	STARD10	-4.95	5.81E-05	7.10E-02	-1.23	-5.66 11q13
37	208892_s_at	DUSP6	2.12	1.83E-03	2.68E-01	1.37	5.66 12q22-q23
38	222984_at	PAIP2	-1.32	2.54E-04	1.18E-01	-1.27	-5.66 5q31.3
39	221952_x_at	KIAA1393	1.39	2.84E-05	6.60E-02	1.20	5.59 14q23.1
40	206614_at	GDF5	-2.83	7.00E-05	7.10E-02	-1.21	-5.56 20q11.2
41	200715_x_at	RPL13A	-1.31	6.18E-03	4.08E-01	-1.48	-5.55 19q13.3
42	215262_at		1.97	3.62E-05	6.60E-02	1.19	5.55
43	225248_at	SPPL2B	-3.23	3.17E-05	6.60E-02	-1.21	-5.46 19p13.3
44	231204_at	FLJ11331	-7.44	2.57E-05	6.60E-02	-1.17	-5.46 4q25
45	214826_at	DKFZp667B1218	2.02	2.41E-03	2.82E-01	1.33	5.43 3p21.2
46	232075_at	REC14	1.62	3.08E-05	6.60E-02	1.16	5.43 15q24.1
47	211747_s_at	LSM5	1.55	3.94E-04	1.43E-01	1.22	5.41 7p14.3
48	213975_s_at	LYZ	1.52	4.82E-05	7.10E-02	1.16	5.41 12q14.3
49	203597_s_at	WBP4	-1.56	3.55E-05	6.60E-02	-1.15	-5.39 13q13.3
50	209981_at	PIPPIN	2.17	1.75E-04	1.06E-01	1.19	5.38 22q13.2- q13.31

2.10 Double versus Status 3

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	236737_at	FLJ31528	2.77	7.41E-13	2.90E-08	2.23	12.26	17q25.3
2	220623_s_at	TSGA10	2.10	2.98E-12	5.83E-08	1.99	11.27	2q11.2
3	205282_at	LRP8	1.73	1.64E-11	2.14E-07	1.96	11.04	1p34
4	225385_s_at	LOC92906	2.61	1.50E-07	1.59E-04	2.06	10.96	2p22.2

5	201382_at	SIP	2.01	7.99E-10	3.91E-06	1.90	10.55	1q24-q25
6	222673_x_at	LOC159090	1.73	2.61E-08	4.65E-05	1.92	10.42	Xq26.3
7	231731_at	OTX2	1.93	2.68E-11	2.63E-07	1.81	10.23	14q21-q22
8	203983_at	TSNAX	1.86	2.27E-07	2.02E-04	1.83	9.79	1q42.1
9	218262_at	FLJ22318	1.64	1.00E-09	3.92E-06	1.73	9.68	5q35.3
10	241536_at		1.94	1.30E-08	3.01E-05	1.74	9.60	
11	243280_at		1.76	3.00E-10	2.35E-06	1.69	9.51	
12	225683_x_at	PHP14	2.53	3.64E-04	2.96E-02	2.01	9.23	9q34.3
13	239246_at		1.97	7.95E-04	4.97E-02	2.09	9.16	
14	222779_s_at	HSA277841	1.54	6.58E-07	4.60E-04	1.71	9.15	17p13.3
15	214038_at	CCL8	2.14	5.93E-09	1.93E-05	1.63	9.08	17q11.2
16	242053_at		1.64	3.49E-07	2.85E-04	1.68	9.07	
17	230438_at	TBX15	1.57	5.55E-10	3.10E-06	1.60	9.06	1p11.1
18	214092_x_at	SFRS14	1.41	4.78E-10	3.10E-06	1.60	9.02	19p12
19	243938_x_at	DNAH5	2.85	1.51E-04	1.68E-02	1.88	9.02	5p15.2
20	237852_at		1.81	6.01E-06	2.07E-03	1.69	8.80	
21	228322_at	C14orf35	2.41	9.71E-10	3.92E-06	1.55	8.77	14q22.2
22	239405_at		1.71	5.41E-09	1.93E-05	1.55	8.70	
23	213911_s_at	H2AFZ	1.45	6.43E-08	9.10E-05	1.56	8.62	4q24
24	232856_at		1.87	1.17E-05	3.28E-03	1.64	8.47	
25	220461_at	FLJ11383	1.72	2.91E-06	1.27E-03	1.58	8.40	1q42.2
26	226944_at	HTRA3	2.29	1.24E-04	1.44E-02	1.68	8.25	4p16.1
27	232075_at	REC14	1.85	1.41E-07	1.53E-04	1.49	8.19	15q24.1
28	233501_at		1.61	8.20E-09	2.36E-05	1.45	8.16	
29	240631_at	MASS1	1.56	9.05E-09	2.36E-05	1.45	8.15	5q13
30	238751_at		2.29	1.42E-08	3.09E-05	1.45	8.14	
31	235766_x_at		1.96	8.58E-09	2.36E-05	1.43	8.09	
32	234938_at	BACH1	2.02	1.57E-03	7.21E-02	1.88	8.09	21q22.11
33	242573_at		2.03	4.71E-04	3.52E-02	1.73	8.08	
34	206245_s_at	NS1-BP	1.79	1.25E-05	3.42E-03	1.53	8.00	1q25.1-q31.1
35	234361_at		2.20	1.30E-04	1.49E-02	1.62	7.99	
36	236396_at		3.48	3.47E-03	1.16E-01	2.00	7.98	
37	221952_x_at	KIAA1393	1.42	5.57E-06	2.02E-03	1.50	7.94	14q23.1
38	202462_s_at	KIAA0801	1.51	1.95E-08	3.82E-05	1.41	7.94	5q31.1
39	233823_at	KIAA1276	2.42	4.54E-06	1.72E-03	1.48	7.87	4p16
40	241655_at		1.91	1.63E-06	8.68E-04	1.45	7.83	
41	214037_s_at	JM1	1.61	1.09E-08	2.67E-05	1.38	7.81	Xp11.23
42	240354_at	MGC35033	1.70	1.72E-08	3.54E-05	1.42	7.78	12q13.11
43	207287_at	FLJ14107	1.72	1.78E-05	4.33E-03	1.48	7.72	8p21.2
44	205083_at	AOX1	1.98	3.50E-06	1.43E-03	1.44	7.71	2q33
45	229812_at	FLJ23277	1.52	1.25E-07	1.49E-04	1.38	7.69	1p36.12
46	205424_at	ProSAPIP2	-4.45	2.23E-08	4.15E-05	-1.38	-7.64	17q21.32
47	236240_at	FLJ21106	1.74	1.14E-07	1.44E-04	1.36	7.60	4q28.1
48	211747_s_at	LSM5	1.67	1.01E-03	5.57E-02	1.67	7.58	7p14.3
49	234682_at		1.63	3.04E-04	2.64E-02	1.57	7.57	
50	218315_s_at	CDK5RAP1	1.33	6.27E-08	9.10E-05	1.34	7.53	20pter-q11.23

2.11 Double versus Status 4

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	215225_s_at	GPR17	5.75	4.09E-06	7.90E-02	6.35	17.64	2q21
2	207201_s_at	SLC22A1	3.51	2.62E-06	7.90E-02	6.07	17.13	6q26
3	222583_s_at	NUP50	3.87	3.77E-05	2.64E-01	5.93	15.55	22q13.31
4	218728_s_at	HSPC163	2.30	4.99E-05	2.64E-01	5.55	14.55	1q42.12
5	237092_at		2.61	8.21E-06	1.06E-01	4.99	14.11	
6	236737_at	FLJ31528	3.89	1.60E-04	3.86E-01	5.72	13.53	17q25.3
7	207114_at	LY6G6C	1.63	1.09E-04	3.79E-01	4.50	11.90	6p21.31
8	206245_s_at	NS1-BP	3.04	2.55E-05	2.46E-01	4.16	11.76	1q25.1- q31.1
9	218538_s_at	MRS2L	1.85	4.16E-05	2.64E-01	3.78	10.70	6p22.3- p22.1
10	202648_at	RPS19	-7.11	2.64E-04	4.52E-01	-4.11	-10.56	19q13.2
11	206244_at	CR1	9.50	6.73E-03	6.74E-01	4.79	10.36	1q32
12	205237_at	FCN1	5.69	5.48E-05	2.64E-01	3.64	10.25	9q34
13	239246_at		2.75	1.28E-04	3.79E-01	3.63	10.15	
14	224839_s_at	GPT2	1.77	8.08E-03	6.77E-01	4.80	10.01	16q12.1
15	218778_x_at	EPS8R1	-5.46	8.36E-05	3.59E-01	-3.48	-9.82	19q13.42
16	218479_s_at	XPO4	1.32	1.25E-04	3.79E-01	3.25	9.17	13q11
17	213851_at		2.70	5.48E-04	4.67E-01	3.34	9.13	
18	214380_at	PRPF31	2.29	5.11E-04	4.67E-01	3.56	9.12	19q13.42
19	223672_at	DKFZp761D221	4.26	2.25E-03	5.63E-01	3.50	9.03	1p31.2
20	223756_at	FLJ10081	5.32	1.21E-03	4.85E-01	3.34	8.92	2p12-p11.2
21	203983_at	TSNAX	2.11	1.58E-04	3.86E-01	3.17	8.84	1q42.1
22	212490_at	DNAJC8	1.35	7.92E-04	4.85E-01	3.59	8.78	1p35.2
23	209515_s_at	RAB27A	3.68	1.25E-04	3.79E-01	3.11	8.76	15q15- q21.1
24	241493_at		4.43	2.16E-04	4.39E-01	3.17	8.74	
25	211747_s_at	LSM5	1.97	4.33E-04	4.67E-01	3.16	8.74	7p14.3
26	211742_s_at	EVI2B	2.09	1.45E-04	3.86E-01	3.01	8.50	17q11.2
27	241394_at		8.61	1.03E-02	6.88E-01	3.89	8.44	
28	223393_s_at	KIAA1474	3.40	3.13E-04	4.52E-01	3.02	8.30	19q12
29	244675_at	RGS8	3.39	5.91E-04	4.67E-01	3.14	8.27	1q25
30	230260_s_at	KIAA0084	3.65	1.29E-03	4.85E-01	3.02	8.17	3p24.3
31	222974_at	IL22	7.62	8.59E-03	6.77E-01	3.54	8.17	12q15
32	217239_x_at		8.65	1.44E-02	6.99E-01	4.36	8.14	
33	210152_at	LILRB4	4.14	2.12E-04	4.39E-01	2.89	8.12	19q13.4
34	205036_at	LSM6	2.27	1.97E-04	4.39E-01	2.88	8.10	4q31.21
35	231216_at		2.54	9.91E-03	6.85E-01	3.47	7.91	
36	232908_at		2.12	3.98E-04	4.67E-01	2.80	7.87	
37	202247_s_at	MTA1	-1.89	2.30E-04	4.44E-01	-2.78	-7.85	14q32.3
38	201540_at	FHL1	-5.17	4.48E-04	4.67E-01	-2.86	-7.83	Xq26
39	200795_at	SPARCL1	2.57	2.92E-03	5.87E-01	2.97	7.78	4q22.1
40	220461_at	FLJ11383	2.14	3.55E-04	4.67E-01	2.79	7.74	1q42.2
41	236239_at		1.37	2.22E-03	5.62E-01	2.89	7.70	
42	207509_s_at	LAIR2	2.16	2.02E-03	5.34E-01	2.87	7.68	19q13.4

43	219251_s_at	FLJ10300	-3.21	3.35E-03	6.17E-01	-2.91	-7.58	7q36.3
44	216406_at		5.56	9.93E-03	6.85E-01	3.26	7.57	
45	234902_s_at	FLJ20557	-5.67	2.88E-04	4.52E-01	-2.68	-7.55	19q13.4
46	237563_s_at		2.09	2.97E-04	4.52E-01	2.67	7.55	
47	234938_at	BACH1	2.31	4.73E-04	4.67E-01	2.68	7.53	21q22.11
48	243317_at		2.49	3.16E-04	4.52E-01	2.68	7.51	
49	240609_at		1.96	3.03E-04	4.52E-01	2.65	7.50	
50	204083_s_at	TPM2	-13.16	1.35E-03	4.85E-01	-2.99	-7.47	9p13.2- p13.1

2.12 Double versus Status 5

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	239567_at		4.97	6.11E-06	1.13E-01	5.20	14.90	
2	202228_s_at	SDFR1	2.28	2.46E-06	9.49E-02	4.77	14.20	15q22
3	220623_s_at	TSGA10	4.10	1.17E-05	1.13E-01	5.03	14.17	2q11.2
4	238481_at	MGP	4.47	1.88E-04	4.53E-01	4.74	13.35	12p13.1- p12.3
5	91816_f_at		1.67	1.17E-04	4.53E-01	4.30	12.37	
6	230420_at		3.86	8.90E-06	1.13E-01	4.05	12.13	
7	232738_at	KIAA1680	6.89	2.01E-03	6.31E-01	3.71	9.84	4q22
8	209981_at	PIPPIN	3.09	5.27E-04	5.17E-01	3.19	9.11	22q13.2- q13.31
9	226035_at	KIAA1203	2.11	4.11E-05	3.17E-01	3.03	9.09	16p12.3
10	207016_s_at	ALDH1A2	3.91	6.96E-05	3.83E-01	3.06	8.98	15q21.2
11	205237_at	FCN1	3.75	5.34E-05	3.43E-01	2.92	8.73	9q34
12	230264_s_at	AP1S2	2.24	9.93E-04	5.73E-01	3.02	8.52	Xp22.31
13	211284_s_at	GRN	2.79	7.13E-03	7.66E-01	3.53	8.51	17q21.32
14	229320_at		1.78	2.41E-03	6.69E-01	2.98	8.12	
15	229812_at	FLJ23277	1.55	9.56E-05	4.53E-01	2.71	8.06	1p36.12
16	235881_at	FHOD2	6.06	7.99E-04	5.25E-01	2.80	8.03	2q23.3
17	229986_at		1.63	1.59E-04	4.53E-01	2.71	7.92	
18	209230_s_at	P8	3.00	1.78E-04	4.53E-01	2.72	7.91	16p11.2
19	206244_at	CR1	4.14	3.10E-03	6.85E-01	2.92	7.87	1q32
20	204493_at	BID	1.87	1.68E-04	4.53E-01	2.63	7.85	22q11.1
21	202462_s_at	KIAA0801	1.56	1.76E-04	4.53E-01	2.68	7.82	5q31.1
22	212412_at		2.23	1.20E-04	4.53E-01	2.59	7.76	
23	222569_at	UGCGL1	1.82	2.23E-04	4.53E-01	2.60	7.72	2q14.3
24	218109_s_at	FLJ14153	1.47	1.98E-04	4.53E-01	2.63	7.67	3q25.32
25	240609_at		1.68	6.21E-04	5.17E-01	2.60	7.58	
26	221156_x_at	CPR8	2.15	1.69E-03	6.13E-01	2.69	7.56	15q21.1
27	243114_at		2.82	1.21E-03	5.97E-01	2.60	7.44	
28	236001_at		1.70	2.21E-04	4.53E-01	2.52	7.39	
29	237714_at		2.31	1.08E-03	5.87E-01	2.54	7.31	
30	212873_at	HA-1	1.69	2.08E-04	4.53E-01	2.46	7.28	19p13.3
31	236898_at		5.08	1.02E-03	5.73E-01	2.50	7.22	
32	237221_at		5.55	4.04E-03	6.93E-01	2.68	7.22	
33	232075_at	REC14	2.01	2.38E-04	4.59E-01	2.45	7.20	15q24.1

34 222779_s_at	HSA277841	1.85	3.46E-04	5.17E-01	2.43	7.06 17p13.3
35 208700_s_at	TKT	1.74	5.35E-04	5.17E-01	2.49	7.01 3p14.3
36 214092_x_at	SFRS14	1.41	6.86E-04	5.17E-01	2.56	7.00 19p12
37 239939_at		1.94	3.86E-03	6.85E-01	2.56	6.99
38 206841_at	PDE6H	5.06	9.61E-03	7.91E-01	2.77	6.91 12p13
39 237563_s_at		1.89	3.01E-04	5.17E-01	2.31	6.90
40 238473_at		2.57	5.74E-04	5.17E-01	2.33	6.89
41 202400_s_at	SRF	-1.58	1.51E-03	5.97E-01	-2.40	-6.89 6p21.1
42 222974_at	IL22	4.65	5.64E-03	7.43E-01	2.58	6.85 12q15
43 231591_at	BHMT	-4.81	8.17E-04	5.25E-01	-2.53	-6.84 5q13.1-q15
44 243189_at		-3.91	5.48E-04	5.17E-01	-2.37	-6.77
45 228176_at	EDG3	5.71	1.31E-03	5.97E-01	2.34	6.76 9q22.1-q22.2
46 202440_s_at	ST5	4.10	1.17E-03	5.97E-01	2.31	6.72 11p15
47 241655_at		3.41	4.99E-04	5.17E-01	2.33	6.72
48 205962_at	PAK2	6.24	1.44E-02	8.00E-01	2.84	6.65 3q29
49 234809_at	HCA127	5.26	1.56E-02	8.00E-01	2.89	6.64 Xq11.1
50 228421_s_at	EFEMP1	5.75	3.34E-03	6.85E-01	2.37	6.59 2p16

2.13 Double versus normal

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	205282_at	LRP8	1.97	1.96E-15	9.31E-12	2.08	15.95	1p34
2	200595_s_at	EIF3S10	1.55	6.14E-14	1.46E-10	1.97	15.01	10q26
3	209206_at	SEC22L1	1.66	1.93E-20	7.33E-16	1.77	14.11	1q21.2-q21.3
4	220623_s_at	TSGA10	2.23	1.62E-18	2.05E-14	1.75	13.84	2q11.2
5	202462_s_at	KIAA0801	1.70	1.95E-10	1.72E-07	1.84	13.61	5q31.1
6	209476_at	TXNDC	1.87	8.96E-17	6.79E-13	1.70	13.37	14q21.3
7	214037_s_at	JM1	1.82	2.53E-15	1.07E-11	1.66	13.00	Xp11.23
8	232075_at	REC14	2.16	7.19E-07	1.01E-04	1.87	12.82	15q24.1
9	213053_at	KIAA0841	1.70	4.83E-17	4.58E-13	1.60	12.68	19q13.11
10	219938_s_at	PSTPIP2	1.81	1.50E-18	2.05E-14	1.56	12.49	18q12
11	224587_at	PC4	1.87	1.79E-05	1.16E-03	1.90	12.18	5p13.3
12	202306_at	POLR2G	1.65	7.03E-08	1.94E-05	1.64	11.72	11q13.1
13	229812_at	FLJ23277	1.81	3.27E-10	2.64E-07	1.54	11.56	1p36.12
14	227442_at	FLJ38991	1.62	6.57E-16	3.76E-12	1.44	11.44	4q13.3
15	218538_s_at	MRS2L	1.98	1.95E-08	6.61E-06	1.54	11.25	6p22.3-p22.1
16	222779_s_at	HSA277841	1.63	4.13E-07	7.00E-05	1.55	10.96	17p13.3
17	219600_s_at	C21orf4	1.81	6.17E-07	9.07E-05	1.56	10.94	21q22.11
18	213737_x_at		1.74	1.69E-09	1.05E-06	1.46	10.89	
19	221471_at	TDE1	1.82	3.30E-13	6.31E-10	1.39	10.86	20q13.1-13.3
20	201382_at	SIP	1.82	2.06E-09	1.24E-06	1.45	10.86	1q24-q25
21	221513_s_at	SDCCAG16	1.55	6.95E-16	3.76E-12	1.36	10.86	Xq26.1
22	205260_s_at	ACYP1	2.31	2.49E-06	2.68E-04	1.53	10.53	14q24.3
23	213312_at	DKFZP586E1923	1.73	4.18E-15	1.59E-11	1.31	10.49	6q15-q16.1

24	201784_s_at	SMAP	1.49	3.82E-14	1.12E-10	1.32	10.45	11p15.1
25	219007_at	Nup43	2.32	1.02E-04	4.10E-03	1.62	10.15	6q24.3
26	203327_at	IDE	1.86	2.09E-06	2.34E-04	1.44	10.02	10q23-q25
27	217746_s_at	PDCD6IP	1.46	4.18E-14	1.13E-10	1.26	10.01	3p22.1
28	238099_at	HSPA4	2.78	1.38E-03	2.88E-02	1.90	9.93	5q31.1-q31.2
29	205446_s_at	ATF2	1.72	8.26E-06	6.67E-04	1.45	9.89	2q32
30	203465_at	MRPL19	1.84	3.73E-14	1.12E-10	1.24	9.89	2q11.1-q11.2
31	200809_x_at	RPL12	-1.18	3.01E-14	1.04E-10	-1.23	-9.87	9q34
32	218109_s_at	FLJ14153	1.67	1.11E-12	1.84E-09	1.25	9.84	3q25.32
33	205588_s_at	FOP	1.66	2.93E-09	1.63E-06	1.29	9.74	6q27
34	221481_x_at	HNRPD	1.41	5.53E-04	1.45E-02	1.69	9.73	4q21.1-q21.2
35	204120_s_at	ADK	2.04	1.10E-03	2.45E-02	1.80	9.73	10cen-q24
36	205424_at	ProSAP1P2	-2.98	4.82E-14	1.22E-10	-1.21	-9.72	17q21.32
37	208374_s_at	CAPZA1	1.49	1.36E-08	5.14E-06	1.28	9.57	1p13.1
38	202228_s_at	SDFR1	1.70	2.36E-11	2.99E-08	1.21	9.47	15q22
39	224444_s_at	MGC14801	2.74	1.11E-03	2.46E-02	1.72	9.42	1q32.2
40	218243_at	RUFY1	1.43	1.83E-10	1.65E-07	1.22	9.39	5q35.3
41	228420_at	PDCD2	1.49	1.84E-08	6.40E-06	1.24	9.31	6q27
42	228322_at	C14orf35	1.97	5.65E-12	7.66E-09	1.18	9.30	14q22.2
43	214092_x_at	SFRS14	1.48	2.61E-13	5.81E-10	1.16	9.29	19p12
44	218870_at	ARHGAP15	1.91	1.03E-05	7.73E-04	1.36	9.28	2q22.2
45	228904_at		1.96	3.33E-13	6.31E-10	1.15	9.23	
46	241330_x_at		-8.85	3.30E-13	6.31E-10	-1.15	-9.21	
47	204798_at	MYB	1.78	1.21E-09	7.90E-07	1.20	9.20	6q22-q23
48	202854_at	HPRT1	1.64	1.76E-04	6.09E-03	1.46	9.14	Xq26.1
49	241086_at		-4.28	5.33E-13	9.62E-10	-1.15	-9.13	
50	201464_x_at	JUN	1.98	1.10E-09	7.29E-07	1.18	9.08	1p32-p31

2.14 Status 1 versus Status 2

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	204383_at	DGCR14	-1.74	1.62E-05	4.70E-01	-0.94	-5.20	22q11.21
2	228495_at		-1.76	6.39E-05	4.70E-01	-0.88	-4.80	
3	214789_x_at	SRP46	1.75	1.36E-04	4.70E-01	0.82	4.48	11q22
4	226321_at	LOC116068	-1.77	1.33E-04	4.70E-01	-0.81	-4.45	5q14.3
5	240153_at		-1.97	1.25E-04	4.70E-01	-0.80	-4.45	
6	235907_at		-1.69	1.33E-04	4.70E-01	-0.80	-4.42	
7	235022_at	MGC24180	-1.62	1.64E-04	4.70E-01	-0.81	-4.40	18p11.1
8	211523_at	GNRHR	-3.31	1.63E-04	4.70E-01	-0.79	-4.37	4q21.2
9	230387_at		-1.83	1.73E-04	4.70E-01	-0.79	-4.34	
10	227045_at		-1.84	3.05E-04	4.70E-01	-0.84	-4.33	
11	241815_at		-1.86	1.68E-04	4.70E-01	-0.78	-4.33	
12	228595_at	HSD17B1	-2.35	1.78E-04	4.70E-01	-0.78	-4.31	17q11-q21
13	217246_s_at	EPAG	-3.33	2.47E-04	4.70E-01	-0.79	-4.27	X
14	234952_s_at	KIAA1542	-2.48	2.66E-04	4.70E-01	-0.79	-4.27	11p15.5

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15	228363_at		-1.70	1.95E-04	4.70E-01	-0.77	-4.27
16	222656_at		-2.15	2.77E-04	4.70E-01	-0.79	-4.25
17	201367_s_at	ZFP36L2	-2.30	2.54E-04	4.70E-01	-0.78	-4.24 2p22.3-p21
18	218522_s_at	VCY2IP1	-1.76	2.31E-04	4.70E-01	-0.76	-4.23 19p13.11
19	201296_s_at	WSB1	-1.63	2.45E-04	4.70E-01	-0.75	-4.19 17q11.1
20	229262_at		-3.55	5.36E-04	5.01E-01	-0.86	-4.16
21	223263_s_at	DKFZP564O1863	-1.91	3.57E-04	4.70E-01	-0.76	-4.14 12p11.23
22	201354_s_at	BAZ2A	-2.05	4.04E-04	4.81E-01	-0.76	-4.13 12q24.3-qter
23	222602_at	FLJ10808	-1.62	3.04E-04	4.70E-01	-0.75	-4.13 4q13.2
24	206796_at	WISP1	-2.46	3.37E-04	4.70E-01	-0.74	-4.08 8q24.1-q24.3
25	205446_s_at	ATF2	-1.89	3.43E-04	4.70E-01	-0.73	-4.07 2q32
26	201164_s_at	PUM1	-1.33	3.44E-04	4.70E-01	-0.73	-4.06 1p35.2
27	221813_at	KIAA1332	-1.93	4.52E-04	5.01E-01	-0.75	-4.05 1p36.23-p36.11
28	226277_at	COL4A3BP	-1.58	3.58E-04	4.70E-01	-0.73	-4.05 5q13.2
29	225753_at	SNX17	-2.16	3.61E-04	4.70E-01	-0.73	-4.04 2p23-p22
30	211048_s_at	ERP70	-1.78	3.67E-04	4.70E-01	-0.73	-4.04 7q35
31	227249_at	NUDE1	-1.61	3.85E-04	4.75E-01	-0.72	-4.02 16p13.11
32	226588_at	KIAA1604	-1.91	5.95E-04	5.05E-01	-0.75	-3.99 2q31.3
33	201389_at	ITGA5	-1.75	4.42E-04	5.01E-01	-0.71	-3.97 12q11-q13
34	238496_at	WHSC1L1	-1.74	5.06E-04	5.01E-01	-0.71	-3.93 8p11.2
35	205574_x_at	BMP1	-1.71	4.97E-04	5.01E-01	-0.70	-3.92 8p21
36	228583_at		-1.70	5.62E-04	5.05E-01	-0.71	-3.91
37	222505_at	C7orf2	-2.22	5.17E-04	5.01E-01	-0.70	-3.91 7q36
38	225858_s_at		-1.60	5.26E-04	5.01E-01	-0.70	-3.91
39	226752_at		-1.64	5.99E-04	5.05E-01	-0.71	-3.91
40	201369_s_at	ZFP36L2	-2.47	7.00E-04	5.12E-01	-0.73	-3.90 2p22.3-p21
41	222414_at	MLL3	-1.41	5.36E-04	5.01E-01	-0.70	-3.90 7q34-q36
42	212748_at	MKL1	-1.60	5.95E-04	5.05E-01	-0.70	-3.87 22q13
43	213244_at	SCAMP-4	-1.92	7.41E-04	5.12E-01	-0.72	-3.86 19p13.3
44	225821_s_at	KIAA1327	-1.63	6.25E-04	5.12E-01	-0.69	-3.84 4p15.33
45	225002_s_at	DKFZP566I1024	-1.59	7.08E-04	5.12E-01	-0.70	-3.84 7q11.1
46	222399_s_at	SMBP	-1.54	6.45E-04	5.12E-01	-0.69	-3.84 10q23.33
47	200014_s_at - HG-U133B	HNRPC	-1.29	7.11E-04	5.12E-01	-0.70	-3.84 14q11.1
48	213066_at	KIAA0375	-2.40	6.67E-04	5.12E-01	-0.70	-3.84 9p13.1
49	243470_at		-2.15	6.58E-04	5.12E-01	-0.69	-3.82
50	234942_s_at		-1.96	8.35E-04	5.42E-01	-0.70	-3.79

2.15 Status 1 versus Status 3

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	209235_at	CLCN7	-3.24	3.11E-06	6.29E-02	-0.87	-5.53	16p13
2	213244_at	SCAMP-4	-2.06	5.21E-06	6.29E-02	-0.83	-5.29	19p13.3
3	217246_s_at	EPAG	-3.22	5.08E-06	6.29E-02	-0.83	-5.29	X
4	242713_at		-2.41	1.67E-05	1.38E-01	-0.78	-4.96	

5	204383_at	DGCR14	-1.58	1.90E-05	1.38E-01	-0.77	-4.92	22q11.21	
6	205574_x_at	BMP1	-1.97	2.73E-05	1.41E-01	-0.74	-4.75	8p21	
7	213066_at	KIAA0375	-2.72	2.81E-05	1.41E-01	-0.74	-4.74	9p13.1	
8	204494_s_at	DKFZP434H132	-2.14	3.10E-05	1.41E-01	-0.74	-4.71	15q22.33	
9	219491_at	MGC3103	-2.76	4.07E-05	1.59E-01	-0.72	-4.63	11q13.1	
10	201079_at	SYNGR2	-1.82	4.38E-05	1.59E-01	-0.72	-4.60	17q25.3	
11	220748_s_at	LOC51157	-1.82	7.28E-05	1.72E-01	-0.73	-4.58	19q13.42	
12	205631_at	KIAA0586	1.37	1.80E-04	1.76E-01	0.79	4.56	14q22.3	
13	201552_at	LAMP1	-1.56	9.55E-05	1.72E-01	-0.73	-4.53	13q34	
14	218438_s_at	EG1	-1.46	5.59E-05	1.72E-01	-0.71	-4.53	4p16	
15	219457_s_at	RIN3	-1.70	8.89E-05	1.72E-01	-0.73	-4.52	14q32.13	
16	236269_at	LOC89887	-1.60	6.00E-05	1.72E-01	-0.70	-4.50		19
17	214394_x_at	EEF1D	-1.31	1.51E-04	1.72E-01	-0.75	-4.50	8q24.3	
18	203891_s_at	DAPK3	-2.13	2.31E-04	1.76E-01	-0.78	-4.50	19p13.3	
19	201329_s_at	ETS2	-2.26	6.43E-05	1.72E-01	-0.70	-4.48	21q22.2	
20	204341_at	TRIM16	-2.07	8.55E-05	1.72E-01	-0.72	-4.48	17p11.2	
21	201487_at	CTSC	-2.05	7.89E-05	1.72E-01	-0.71	-4.48	11q14.1-q14.3	
22	214698_at	ROD1	-1.75	1.57E-04	1.72E-01	-0.73	-4.42	9q32	
23	212300_at	DKFZp451J0118	-1.71	8.63E-05	1.72E-01	-0.69	-4.41	1p34.3	
24	216180_s_at		-7.20	1.32E-04	1.72E-01	-0.76	-4.40		
25	234408_at	IL17F	-2.31	1.02E-04	1.72E-01	-0.70	-4.40	6p12	
26	238203_at		-2.81	9.13E-05	1.72E-01	-0.68	-4.36		
27	227355_at		1.76	2.84E-04	1.76E-01	0.73	4.32		
28	225753_at	SNX17	-2.08	1.66E-04	1.72E-01	-0.70	-4.32	2p23-p22	
29	227469_at	PTEN	1.25	1.26E-04	1.72E-01	0.68	4.31	10q23.3	
30	209308_s_at	BNIP2	-1.57	1.92E-04	1.76E-01	-0.70	-4.30	15q21.3	
31	205774_at	F12	-1.78	1.56E-04	1.72E-01	-0.68	-4.28	5q33-qter	
32	201551_s_at	LAMP1	-1.65	1.22E-04	1.72E-01	-0.67	-4.27	13q34	
33	234952_s_at	KIAA1542	-2.06	1.25E-04	1.72E-01	-0.67	-4.26	11p15.5	
34	224453_s_at	EKI1	-1.80	1.26E-04	1.72E-01	-0.67	-4.26	12p12.1	
35	225254_at	MGC20255	-1.97	1.76E-04	1.76E-01	-0.68	-4.25	19q13.13	
36	219681_s_at	RCP	-1.95	1.31E-04	1.72E-01	-0.66	-4.25	8p11.22	
37	202682_s_at	USP4	-1.38	1.34E-04	1.72E-01	-0.66	-4.24	3p21.3	
38	220516_at	ZFP29	-2.53	1.51E-04	1.72E-01	-0.67	-4.24	15q25.1	
39	212005_at	DKFZP566C0424	-2.96	1.59E-04	1.72E-01	-0.65	-4.18	1p36.13	
40	224669_at	C20orf169	-1.37	1.65E-04	1.72E-01	-0.65	-4.17	20q13.11	
41	221754_s_at	CORO1B	-2.89	3.36E-04	1.76E-01	-0.68	-4.14	11q13.1	
42	205281_s_at	PIGA	-1.79	2.20E-04	1.76E-01	-0.65	-4.11	Xp22.1	
43	204090_at	STK19	-1.42	3.99E-04	1.84E-01	-0.68	-4.11	6p21.3	
44	217411_s_at	RREB1	-3.16	2.10E-04	1.76E-01	-0.65	-4.11	6p25	
45	224439_x_at	RNF7	-1.51	2.20E-04	1.76E-01	-0.64	-4.09	3q22-q24	
46	218964_at	DRIL2	-2.57	2.14E-04	1.76E-01	-0.64	-4.09	15q24	
47	222488_s_at	DCTN4	-1.56	2.48E-04	1.76E-01	-0.64	-4.08	5q31-q32	
48	207118_s_at	MMP23A	-2.34	2.51E-04	1.76E-01	-0.65	-4.08	1p36.3	
49	205227_at	IL1RAP	-2.58	2.82E-04	1.76E-01	-0.65	-4.08	3q28	
50	201585_s_at	SFPQ	-1.55	2.23E-04	1.76E-01	-0.64	-4.07	1p34.3	

2.16 Status 1 versus Status 4

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	219964_at	ST7L	-2.73	9.88E-07	2.65E-02	-2.06	-8.42	1p13.1
2	36545_s_at	KIAA0542	-1.66	1.65E-06	2.65E-02	-1.93	-7.90	22q12.2
3	240943_at		-3.91	3.82E-04	1.37E-01	-2.31	-7.81	
4	201551_s_at	LAMP1	-1.90	3.05E-05	9.31E-02	-1.91	-7.48	13q34
5	242313_at		-2.52	2.64E-04	1.16E-01	-2.08	-7.42	
6	202648_at	RPS19	-4.11	2.87E-05	9.31E-02	-1.87	-7.36	19q13.2
7	201005_at	CD9	-5.45	1.72E-04	1.16E-01	-1.98	-7.29	12p13.3
8	206799_at	SCGB1D2	2.06	2.88E-06	3.08E-02	1.77	7.26	11q13
9	218983_at	LOC51279	-2.86	3.52E-05	9.31E-02	-1.85	-7.24	12p13.31
10	221942_s_at	GUCY1A3	-3.18	6.47E-05	9.44E-02	-1.86	-7.19	4q31.1- q31.2
11	210425_x_at	GOLGIN-67	-2.52	1.22E-04	1.16E-01	-1.84	-6.98	15q11.2
12	204341_at	TRIM16	-2.48	9.36E-04	1.71E-01	-2.12	-6.91	17p11.2
13	201862_s_at	LRRFIP1	-1.88	5.60E-05	9.31E-02	-1.73	-6.81	2q37.3
14	220974_x_at	BA108L7.2	-3.88	5.88E-05	9.31E-02	-1.70	-6.69	10q24.31
15	45297_at	MGC45806	-4.32	1.15E-03	1.87E-01	-2.06	-6.67	1p35.2
16	204073_s_at	C11orf9	-3.14	2.23E-04	1.16E-01	-1.72	-6.49	11q12- q13.1
17	205774_at	F12	-2.71	4.49E-04	1.39E-01	-1.79	-6.48	5q33-qter
18	200768_s_at	MAT2A	-1.85	1.67E-05	9.31E-02	-1.57	-6.44	2p11.2
19	206574_s_at	PTP4A3	-7.94	1.51E-03	1.95E-01	-2.00	-6.40	
20	201613_s_at	RUVBL1	-2.69	2.15E-04	1.16E-01	-1.68	-6.39	3q21
21	227227_at		-2.04	1.96E-05	9.31E-02	-1.56	-6.38	
22	217226_s_at	BA108L7.2	-3.12	5.75E-04	1.47E-01	-1.77	-6.34	10q24.31
23	201552_at	LAMP1	-1.82	4.50E-05	9.31E-02	-1.57	-6.31	13q34
24	202111_at	SLC4A2	-7.13	1.41E-03	1.94E-01	-1.89	-6.24	7q35-q36
25	221005_s_at	PTDSS2	-1.94	2.01E-05	9.31E-02	-1.48	-6.12	11p15
26	225180_at	FLJ00166	-2.24	6.09E-05	9.31E-02	-1.51	-6.09	3q27.2
27	212608_s_at		-1.85	2.23E-05	9.31E-02	-1.48	-6.08	
28	223716_s_at	ZNF265	-1.90	1.50E-04	1.16E-01	-1.53	-6.00	1p31
29	218518_at	C5orf5	-1.80	5.80E-05	9.31E-02	-1.48	-5.99	5q31
30	226959_at		-3.41	6.44E-04	1.49E-01	-1.64	-5.98	
31	202344_at	HSF1	-1.65	2.65E-05	9.31E-02	-1.45	-5.96	8q24.3
32	222138_s_at	WDR13	-1.97	1.05E-03	1.82E-01	-1.69	-5.94	Xp11.23
33	230589_at		-2.50	4.72E-05	9.31E-02	-1.44	-5.90	
34	237243_at		-3.09	4.37E-04	1.37E-01	-1.55	-5.86	
35	202247_s_at	MTA1	-1.58	2.46E-04	1.16E-01	-1.50	-5.84	14q32.3
36	229700_at		-2.37	1.13E-03	1.87E-01	-1.65	-5.81	
37	209695_at	PTP4A3	-2.46	1.75E-03	1.98E-01	-1.73	-5.81	
38	208728_s_at	CDC42	-1.78	5.77E-05	9.31E-02	-1.41	-5.77	1p36.1
39	206148_at	IL3RA	-6.45	3.21E-03	2.28E-01	-1.93	-5.75	Xp22.3 or Yp11.3
40	231896_s_at	DENR	-1.64	5.90E-05	9.31E-02	-1.40	-5.72	12q24.31
41	230434_at	MGC22679	-2.10	1.77E-04	1.16E-01	-1.44	-5.72	2q31.1
42	212176_at	DKFZp564B0769	-1.85	1.19E-04	1.16E-01	-1.42	-5.71	6q16.3

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43	203085_s_at	TGFB1	-2.52	2.37E-04	1.16E-01	-1.45	-5.70	19q13.2
44	209742_s_at	MYL2	3.30	5.30E-05	9.31E-02	1.39	5.67	12q23-q24.3
45	204160_s_at	ENPP4	-2.45	3.00E-04	1.24E-01	-1.45	-5.65	6p12.3
46	219595_at	ZNF26	-1.46	1.16E-04	1.16E-01	-1.46	-5.63	12q24.33
47	242832_at	PER1	-2.70	7.16E-05	9.58E-02	-1.37	-5.59	17p13.1-17p12
48	235780_at	PRKACB	-2.03	5.54E-05	9.31E-02	-1.36	-5.59	1p36.1
49	201260_s_at	SYPL	-1.57	1.54E-04	1.16E-01	-1.39	-5.56	7q22.1
50	213851_at		2.56	6.78E-05	9.46E-02	1.36	5.55	

2.17 Status 1 versus Status 5

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	213244_at	SCAMP-4	-2.80	1.26E-03	8.94E-01	-1.69	-5.69	19p13.3
2	203453_at	SCNN1A	4.02	1.28E-04	8.94E-01	1.45	5.59	12p13
3	201329_s_at	ETS2	-2.27	8.14E-05	8.94E-01	-1.32	-5.52	21q22.2
4	209742_s_at	MYL2	2.53	1.87E-04	8.94E-01	1.32	5.24	12q23-q24.3
5	241821_at		2.20	1.40E-04	8.94E-01	1.19	5.00	
6	241909_at		11.41	3.79E-04	8.94E-01	1.35	5.00	
7	239567_at		3.46	1.72E-04	8.94E-01	1.16	4.89	
8	234234_at		2.46	2.56E-04	8.94E-01	1.16	4.81	
9	31846_at	ARHD	1.47	3.09E-04	8.94E-01	1.15	4.79	11q14.3
10	228992_at	EG1	-1.40	2.91E-04	8.94E-01	-1.14	-4.78	4p16
11	217575_s_at	SOS2	3.75	4.34E-04	8.94E-01	1.21	4.77	14q21
12	221201_s_at	ZNF155	-3.31	2.51E-03	8.94E-01	-1.29	-4.64	19q13.2-q13.32
13	204105_s_at	NRCAM	2.40	5.34E-04	8.94E-01	1.08	4.50	7q31.1-q31.2
14	227355_at		2.35	7.44E-04	8.94E-01	1.10	4.50	
15	208007_at		3.82	6.81E-04	8.94E-01	1.13	4.49	
16	213778_x_at	FANCA	-1.60	4.35E-04	8.94E-01	-1.06	-4.49	16q24.3
17	210158_at	ERCC4	2.64	3.90E-04	8.94E-01	1.05	4.47	16p13.3-p13.11
18	222734_at	WARS2	-1.78	1.73E-03	8.94E-01	-1.15	-4.46	1p13.3-p13.1
19	231010_at	PRO0971	1.84	6.01E-04	8.94E-01	1.09	4.45	4q25
20	226415_at	KIAA1576	3.09	4.91E-04	8.94E-01	1.06	4.44	16q23.1
21	202646_s_at	D1S155E	-1.38	4.65E-04	8.94E-01	-1.05	-4.43	1p22
22	226585_at	NEIL2	-2.14	8.75E-04	8.94E-01	-1.08	-4.43	
23	225389_at	BTBD6	1.55	4.98E-04	8.94E-01	1.05	4.41	14q32
24	208519_x_at	GNRH2	2.16	5.89E-04	8.94E-01	1.05	4.41	20p13
25	228950_s_at	FLJ23091	4.03	1.05E-03	8.94E-01	1.17	4.36	1p31.2
26	200606_at	DSP	2.23	7.22E-04	8.94E-01	1.05	4.36	6p24
27	219488_at	A4GALT	2.01	5.50E-04	8.94E-01	1.02	4.31	22q11.2-q13.2
28	238267_s_at		2.91	5.88E-04	8.94E-01	1.02	4.30	
29	206159_at	GDF10	3.13	7.86E-04	8.94E-01	1.03	4.25	10q11.21
30	222178_s_at	CDC5L	3.40	7.79E-04	8.94E-01	1.02	4.24	6p21

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31 243875_at		2.37	1.20E-03	8.94E-01	1.03	4.24
32 221339_at		2.02	3.46E-03	8.94E-01	1.13	4.20
33 213140_s_at	SS18L1	-1.52	1.11E-03	8.94E-01	-1.00	-4.17 20q13.3
34 240720_at		2.43	2.43E-03	8.94E-01	1.06	4.16
35 205318_at	KIF5A	1.51	7.85E-04	8.94E-01	0.98	4.15 12q13
36 218965_s_at	FLJ22347	3.04	1.06E-03	8.94E-01	1.01	4.15 11q12.2
37 46256_at	SSB3	1.58	8.34E-04	8.94E-01	0.98	4.14 16p13.3
38 232170_at	S100A15	2.55	8.80E-04	8.94E-01	0.99	4.13
39 244692_at	FLJ39501	3.16	8.34E-04	8.94E-01	0.97	4.11 19p13.11
40 214424_s_at	ALDOB	2.44	8.57E-04	8.94E-01	0.97	4.11 9q21.3-q22.2
41 232025_at	PCANAP7	1.93	8.53E-04	8.94E-01	0.97	4.11 11q12.2
42 201524_x_at	UBE2N	-1.29	1.88E-03	8.94E-01	-1.01	-4.10 12q22
43 242656_at	GTF2H1	2.80	8.46E-04	8.94E-01	0.97	4.10 11p15.1-p14
44 243564_at		2.97	1.30E-03	8.94E-01	1.02	4.10
45 236353_at		4.18	8.83E-04	8.94E-01	0.97	4.09
46 228429_x_at	KIF9	-1.57	1.71E-03	8.94E-01	-1.01	-4.09 3p21.31
47 AFFX-r2-Ec-bioD-3_at - HG-U133B		1.40	8.76E-04	8.94E-01	0.96	4.08
48 230987_at		2.21	8.87E-04	8.94E-01	0.96	4.07
49 215044_s_at	STAM2	1.48	8.88E-04	8.94E-01	0.96	4.07 2q23.3
50 214823_at	ZNF204	2.37	1.35E-03	8.94E-01	1.01	4.07 6p21.3

2.18 Status 1 versus normal

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	237243_at		-3.49	2.63E-07	5.39E-03	-0.67	-5.70	
2	208145_at	FLJ20802	-3.20	3.23E-07	5.39E-03	-0.67	-5.67	20p13
3	211523_at	GNRHR	-3.13	2.67E-06	1.27E-02	-0.68	-5.45	4q21.2
4	223346_at	VPS18	-1.79	2.18E-06	1.21E-02	-0.66	-5.39	15q14-q15
5	205013_s_at	ADORA2A	-2.07	1.07E-06	1.19E-02	-0.63	-5.35	22q11.23
6	218059_at	LOC51123	-1.47	1.99E-06	1.21E-02	-0.62	-5.24	8q22.3
7	201460_at	MAPKAPK2	-1.51	7.91E-06	2.03E-02	-0.65	-5.19	1q32
8	223441_at	SLC17A5	-2.08	2.07E-06	1.21E-02	-0.61	-5.17	6q14-q15
9	204383_at	DGCR14	-1.50	1.73E-05	2.50E-02	-0.68	-5.17	22q11.21
10	217246_s_at	EPAG	-2.88	4.89E-06	1.81E-02	-0.62	-5.14	X
11	228812_at		-1.96	1.11E-05	2.17E-02	-0.63	-5.06	
12	233888_s_at	SRGAP1	-2.79	3.37E-06	1.40E-02	-0.59	-5.05	12q14.1
13	208072_s_at	DGKD	-1.93	6.78E-06	1.88E-02	-0.60	-5.01	2q37.1
14	213749_at	MASP1	-2.17	1.55E-05	2.40E-02	-0.62	-4.95	3q27-q28
15	213961_s_at	TAF6L	-1.96	6.61E-06	1.88E-02	-0.58	-4.90	11q12.2
16	239925_at		-2.01	6.65E-06	1.88E-02	-0.57	-4.87	
17	236683_at		-1.76	2.82E-05	2.82E-02	-0.62	-4.85	
18	206235_at	LIG4	-1.85	1.06E-05	2.17E-02	-0.58	-4.83	13q33-q34
19	211122_s_at	CXCL11	-2.99	1.24E-05	2.21E-02	-0.58	-4.80	4q21.2
20	216982_x_at		-3.04	9.07E-06	2.16E-02	-0.57	-4.80	
21	203761_at	SLA	-2.26	1.07E-05	2.17E-02	-0.56	-4.78	8q24

22 204872_at	BCE-1	-1.75	1.44E-05	2.40E-02	-0.57	-4.74	9q21.31
23 213033_s_at		-1.70	1.58E-05	2.40E-02	-0.57	-4.73	
24 219582_at	FLJ21079	-1.63	2.25E-05	2.75E-02	-0.58	-4.72	6q13
25 220569_at	PRO1728	-1.97	1.26E-05	2.21E-02	-0.56	-4.72	10q21.1
26 231981_at		-1.75	2.87E-05	2.82E-02	-0.58	-4.69	
27 228087_at	LOC90693	-1.74	4.72E-05	3.30E-02	-0.59	-4.67	7p15.3
28 244115_at	DRCTNNB1A	-2.25	2.07E-05	2.66E-02	-0.55	-4.64	7p15.3
29 242541_at	ABCA9	-1.92	4.45E-05	3.30E-02	-0.58	-4.63	17q24.2
30 46323_at	SHAPY	-1.43	5.14E-05	3.30E-02	-0.59	-4.62	17q25.3
31 226566_at	TRIM11	-1.63	1.94E-05	2.59E-02	-0.54	-4.61	1q42.13
32 212117_at	TC10	-1.52	2.96E-05	2.82E-02	-0.56	-4.60	2p21
33 220363_s_at	ELMO2	-3.55	1.93E-05	2.59E-02	-0.54	-4.60	20q13
34 221697_at		-2.28	2.69E-05	2.80E-02	-0.55	-4.59	
35 222205_x_at		-2.07	6.58E-05	3.30E-02	-0.59	-4.59	
36 233000_x_at	C20orf143	-1.75	3.20E-05	2.88E-02	-0.55	-4.58	20q13.33
37 228363_at		-1.63	5.53E-05	3.30E-02	-0.58	-4.57	
38 204495_s_at	DKFZP434H132	-1.82	5.21E-05	3.30E-02	-0.57	-4.57	15q22.33
39 216181_at		-1.55	6.63E-05	3.30E-02	-0.58	-4.55	
40 221840_at	PTPRE	-1.94	5.16E-05	3.30E-02	-0.56	-4.54	10q26
41 222415_at	MLL3	-1.61	2.43E-05	2.75E-02	-0.53	-4.53	7q34-q36
42 218284_at	DKFZP586N0721	-1.89	2.55E-05	2.75E-02	-0.53	-4.52	15q22.2
43 220900_at	FLJ12078	-3.76	2.53E-05	2.75E-02	-0.53	-4.51	5q14.3
44 244549_at		-2.05	6.82E-05	3.30E-02	-0.57	-4.51	
45 214266_s_at	ENIGMA	-2.57	2.51E-05	2.75E-02	-0.53	-4.51	5q35.3
46 215575_at		-2.79	3.73E-05	3.18E-02	-0.54	-4.50	
47 228234_at		-2.17	4.64E-05	3.30E-02	-0.55	-4.49	
48 201110_s_at	THBS1	-6.24	3.15E-05	2.88E-02	-0.54	-4.48	15q15
49 217191_x_at		-1.62	2.11E-04	4.72E-02	-0.63	-4.48	
50 218728_s_at	HSPC163	-1.80	6.29E-05	3.30E-02	-0.56	-4.47	1q42.12

2.19 Status 2 versus Status 3

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	213048_s_at	SET	-1.52	6.56E-05	5.93E-01	-0.65	-4.44	9q34
2	201150_s_at	TIMP3	2.10	2.09E-04	5.93E-01	0.65	4.20	22q12.3
3	215139_at		2.10	2.60E-04	5.93E-01	0.65	4.16	
4	212619_at	KIAA0286	1.54	2.98E-04	5.93E-01	0.63	4.09	12q13.13
5	208958_at	TXNDC4	1.97	4.76E-04	5.93E-01	0.66	4.03	9q22.33
6	239413_at		1.83	6.26E-04	5.93E-01	0.70	4.00	
7	204413_at	TRAF2	2.25	4.83E-04	5.93E-01	0.64	3.99	9q34
8	215170_s_at	KIAA0912	2.20	6.46E-04	5.93E-01	0.66	3.94	15q15.2
9	228583_at		1.63	6.77E-04	5.93E-01	0.66	3.93	
10	222702_x_at	CRIP1	1.51	6.66E-04	5.93E-01	0.63	3.88	2p21
11	213736_at	COX5B	-2.86	5.52E-04	5.93E-01	-0.57	-3.79	2cen-q13
12	226601_at		1.52	7.93E-04	5.93E-01	0.60	3.79	
13	227942_s_at	CRIP1	1.45	1.25E-03	5.93E-01	0.61	3.66	2p21

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14	235719_at		-1.88	6.61E-04	5.93E-01	-0.53	-3.66
15	215487_x_at		-2.08	7.76E-04	5.93E-01	-0.52	-3.60
16	219920_s_at	GMPPB	1.49	1.07E-03	5.93E-01	0.54	3.57 3p21.31
17	207688_s_at	INHBC	-1.65	8.81E-04	5.93E-01	-0.52	-3.56 12q13.1
18	215106_at	FLJ20619	2.03	1.22E-03	5.93E-01	0.53	3.53 1p32.2
19	202028_s_at	RPL38	-1.72	1.20E-03	5.93E-01	-0.51	-3.48 17q23-q25
20	216450_x_at	TRA1	-1.47	1.26E-03	5.93E-01	-0.50	-3.46 12q24.2-q24.3
21	244324_at		2.32	2.41E-03	5.93E-01	0.60	3.44
22	219758_at	FLJ12571	1.74	1.56E-03	5.93E-01	0.51	3.43 7q34
23	232065_x_at	dJ383J4.3	1.80	2.71E-03	5.93E-01	0.62	3.42 1q23.3
24	235952_at		2.45	1.80E-03	5.93E-01	0.52	3.42
25	216180_s_at		-3.55	1.57E-03	5.93E-01	-0.51	-3.41
26	226089_at	MGC23920	1.48	2.29E-03	5.93E-01	0.56	3.41 3q13.33
27	235089_at	MGC15482	1.61	2.75E-03	5.93E-01	0.61	3.40 17q21.1
28	241522_at		1.65	1.52E-03	5.93E-01	0.49	3.38
29	235549_at	LOC255488	2.59	2.42E-03	5.93E-01	0.55	3.37 6p22.3
30	215450_at	SNRPE	-1.53	1.83E-03	5.93E-01	-0.49	-3.33 1q32
31	204329_s_at	ZNF202	2.10	2.74E-03	5.93E-01	0.54	3.33 11q23.3
32	234216_at		-1.44	1.75E-03	5.93E-01	-0.48	-3.32
33	244193_at	FLJ13236	1.43	2.58E-03	5.93E-01	0.52	3.31 12q13.12
34	237293_at		2.05	2.73E-03	5.93E-01	0.53	3.31
35	218009_s_at	PRC1	1.57	3.15E-03	5.93E-01	0.55	3.30 15q26.1
36	205631_at	KIAA0586	1.33	2.88E-03	5.93E-01	0.53	3.29 14q22.3
37	226544_x_at	MU	1.49	2.85E-03	5.93E-01	0.52	3.28 6p25.1-p24.3
38	237942_at	SNRK	-1.45	2.51E-03	5.93E-01	-0.50	-3.27 3p21.32
39	225888_at	FLJ13089	1.71	3.78E-03	5.93E-01	0.58	3.26 12q24.13
40	212005_at	DKFZP566C0424	-1.99	2.22E-03	5.93E-01	-0.47	-3.25 1p36.13
41	217213_at		2.04	3.58E-03	5.93E-01	0.55	3.25
42	202648_at	RPS19	-2.18	2.37E-03	5.93E-01	-0.47	-3.22 19q13.2
43	219036_at	BITE	-2.00	2.66E-03	5.93E-01	-0.48	-3.22 3q22-q23
44	238149_at		1.74	3.27E-03	5.93E-01	0.51	3.22
45	203174_s_at	ARFRP1	1.58	2.81E-03	5.93E-01	0.48	3.22 20q13.3
46	231027_at		1.61	2.55E-03	5.93E-01	0.47	3.21
47	219444_at	FLJ11362	1.50	3.56E-03	5.93E-01	0.51	3.20 Xq25-q26.1
48	212740_at	PIK3R4	1.49	3.69E-03	5.93E-01	0.51	3.18 3q22.1
49	236589_at		1.60	3.19E-03	5.93E-01	0.48	3.17
50	238737_at	FLJ32112	2.10	4.82E-03	5.93E-01	0.58	3.17 1p32.3

2.20 Status 2 versus Status 4

#	affy id	HUGO name	fc	p	q	strn	t	Map Location
1	217526_at		-1.69	2.56E-05	6.08E-02	-1.79	-7.85	
2	201005_at	CD9	-5.57	2.79E-04	8.82E-02	-1.99	-7.69	12p13.3
3	202648_at	RPS19	-3.77	2.71E-05	6.08E-02	-1.59	-7.16	19q13.2
4	219833_s_at	FLJ10466	-1.94	2.89E-05	6.08E-02	-1.55	-7.01	6p12.1

5	45297_at	MGC45806	-4.54	1.10E-03	1.48E-01	-1.93	-6.79 1p35.2
6	203227_s_at	SAS	-1.87	2.64E-05	6.08E-02	-1.44	-6.62 12q13.3
7	231896_s_at	DENR	-1.55	1.05E-04	6.71E-02	-1.50	-6.58 12q24.31
8	213359_at		-1.57	1.92E-06	3.57E-02	-1.33	-6.49
9	210425_x_at	GOLGIN-67	-2.41	9.57E-05	6.71E-02	-1.47	-6.49 15q11.2
10	201280_s_at	DAB2	-2.42	6.86E-04	1.18E-01	-1.66	-6.46 5p13
11	211578_s_at	RPS6KB1	2.86	2.30E-06	3.57E-02	1.32	6.43 17q23.2
12	210613_s_at	SYNGR1	3.04	1.09E-05	5.81E-02	1.35	6.42 22q13.1
13	226959_at		-3.53	9.00E-04	1.37E-01	-1.68	-6.39
14	221942_s_at	GUCY1A3	-2.80	5.36E-05	6.65E-02	-1.35	-6.20 4q31.1- q31.2
15	212221_x_at		-2.35	4.12E-04	1.01E-01	-1.46	-6.10
16	36545_s_at	KIAA0542	-1.55	7.02E-06	5.81E-02	-1.22	-5.95 22q12.2
17	210129_s_at	DKFZP434B103	-1.76	9.01E-05	6.71E-02	-1.30	-5.93 3p25.3
18	204895_x_at	MUC4	4.15	1.13E-05	5.81E-02	1.28	5.92 3q29
19	230589_at		-2.68	1.69E-05	5.81E-02	-1.23	-5.91
20	227115_at		-1.83	4.50E-05	6.35E-02	-1.24	-5.84
21	39248_at	AQP3	-3.61	1.82E-03	1.75E-01	-1.60	-5.84 9p13
22	215946_x_at	LOC91316	2.88	1.67E-05	5.81E-02	1.27	5.78 22q11.21
23	222078_at	HCN3	3.06	8.82E-06	5.81E-02	1.18	5.76 1q21.3
24	218983_at	LOC51279	-2.06	1.87E-04	7.46E-02	-1.28	-5.75 12p13.31
25	213317_at		-2.18	1.15E-04	6.71E-02	-1.22	-5.63
26	238886_at		-2.42	2.48E-04	8.18E-02	-1.26	-5.62
27	228476_at	KIAA1407	-2.69	6.16E-04	1.15E-01	-1.31	-5.56 3q13.2
28	219251_s_at	FLJ10300	-2.19	1.45E-05	5.81E-02	-1.13	-5.54 7q36.3
29	213785_at		-2.02	7.22E-04	1.22E-01	-1.32	-5.53
30	222583_s_at	NUP50	2.69	2.59E-05	6.08E-02	1.14	5.52 22q13.31
31	221509_at	DENR	-1.50	1.54E-04	7.06E-02	-1.19	-5.49 12q24.31
32	213048_s_at	SET	-2.02	3.21E-03	1.97E-01	-1.58	-5.44 9q34
33	220974_x_at	BA108L7.2	-2.32	4.64E-04	1.04E-01	-1.25	-5.44 10q24.31
34	212608_s_at		-1.70	2.94E-05	6.08E-02	-1.11	-5.39
35	202792_s_at	KIAA0685	-1.93	1.15E-04	6.71E-02	-1.15	-5.37 22q13.33
36	207129_at	CA5B	-2.32	1.54E-03	1.69E-01	-1.36	-5.37 Xp21.1
37	222138_s_at	WDR13	-1.86	1.12E-03	1.48E-01	-1.30	-5.35 Xp11.23
38	228331_at	SELH	-1.74	4.21E-05	6.35E-02	-1.10	-5.34
39	206574_s_at	PTP4A3	-3.83	2.85E-03	1.90E-01	-1.48	-5.34
40	200918_s_at	SRPR	1.48	4.04E-05	6.35E-02	1.10	5.32 11q24.3
41	235549_at	LOC255488	9.44	4.16E-05	6.35E-02	1.15	5.32 6p22.3
42	225180_at	FLJ00166	-1.87	2.01E-04	7.74E-02	-1.15	-5.29 3q27.2
43	210248_at	WNT7A	2.69	3.17E-05	6.15E-02	1.09	5.28 3p25
44	220341_s_at	LOC51149	-1.78	1.10E-04	6.71E-02	-1.11	-5.23 5q35.3
45	208978_at	CRIP2	-6.46	4.13E-03	2.06E-01	-1.56	-5.22 14q32.3
46	214675_at	KIAA0169	-2.03	8.18E-05	6.71E-02	-1.09	-5.21 9q34.13
47	224664_at	LOC119504	-1.79	2.06E-03	1.80E-01	-1.33	-5.18 10q22.1
48	202822_at	LPP	-1.66	4.75E-04	1.04E-01	-1.16	-5.16 3q27-q28
49	202371_at	FLJ21174	-1.60	3.73E-05	6.35E-02	-1.05	-5.14 Xq22.1
50	211727_s_at	COX11	-1.66	4.51E-04	1.04E-01	-1.14	-5.12 17q22

2.21 Status 2 versus Status 5

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	206204_at	GRB14	7.18	3.17E-06	9.71E-02	1.41	6.54	2q22-q24
2	214819_at	KIAA0522	3.91	5.10E-06	9.71E-02	1.18	5.91	Xp11.22
3	205318_at	KIF5A	1.55	2.23E-05	2.83E-01	1.10	5.44	12q13
4	205666_at	FMO1	3.55	1.19E-04	4.84E-01	1.05	5.06	1q23-q25
5	219736_at	TRIM36	9.02	8.29E-05	4.84E-01	1.05	4.97	5q22.2
6	208007_at		3.50	9.90E-05	4.84E-01	0.98	4.79	
7	225410_at		1.50	1.27E-04	4.84E-01	0.97	4.71	
8	203673_at	TG	2.42	9.94E-05	4.84E-01	0.94	4.70	8q24.2-q24.3
9	220542_s_at	PLUNC	2.11	1.05E-04	4.84E-01	0.94	4.68	20q11.2
10	211856_x_at	CD28	2.57	1.06E-04	4.84E-01	0.93	4.67	2q33
11	217329_x_at		1.75	6.89E-04	6.06E-01	1.02	4.65	
12	215396_at	MASS1	3.75	4.09E-04	6.06E-01	0.98	4.64	5q13
13	233679_at		2.02	5.26E-04	6.06E-01	0.97	4.55	
14	216651_s_at	GAD2	3.37	3.63E-04	6.06E-01	0.93	4.49	10p11.23
15	227514_at		1.50	2.55E-04	6.06E-01	0.92	4.44	
16	209456_s_at	FBXW1B	1.94	7.22E-04	6.06E-01	0.95	4.43	5q35.1
17	216978_x_at		4.23	3.27E-04	6.06E-01	0.96	4.40	
18	210158_at	ERCC4	2.80	2.21E-04	6.06E-01	0.88	4.38	16p13.3-p13.11
19	222765_x_at	C20orf6	1.91	2.37E-04	6.06E-01	0.87	4.35	20p12.1
20	217177_s_at		2.35	2.46E-04	6.06E-01	0.87	4.35	
21	210721_s_at	PAK7	4.54	3.59E-04	6.06E-01	0.87	4.25	20p12
22	235549_at	LOC255488	4.25	3.29E-04	6.06E-01	0.85	4.24	6p22.3
23	208061_at	LOC51045	3.78	3.58E-04	6.06E-01	0.86	4.23	
24	235187_s_at		3.04	3.79E-04	6.06E-01	0.86	4.22	
25	235526_at		3.49	3.83E-04	6.06E-01	0.85	4.20	
26	238269_at		2.06	1.63E-03	6.31E-01	0.93	4.19	
27	226347_at		1.67	3.79E-04	6.06E-01	0.83	4.16	
28	214711_at	15E1.2	2.23	6.52E-04	6.06E-01	0.85	4.16	12q24.31
29	226585_at	NEIL2	-1.89	1.77E-03	6.31E-01	-0.92	-4.15	
30	228810_at	FLJ40432	1.59	4.10E-04	6.06E-01	0.83	4.14	2q34
31	239818_x_at		1.84	5.90E-04	6.06E-01	0.84	4.12	
32	230982_at		3.52	4.18E-04	6.06E-01	0.82	4.12	
33	220405_at	SNTG1	2.54	5.20E-04	6.06E-01	0.83	4.10	8q11-q12
34	212763_at	KIAA1078	1.86	7.65E-04	6.06E-01	0.84	4.10	1q31.3
35	211466_at	NFIB	5.35	6.14E-04	6.06E-01	0.86	4.08	9p24.1
36	206361_at	GPR44	2.15	1.11E-03	6.06E-01	0.85	4.05	11q12-q13.3
37	220776_at	KCNJ14	2.40	2.53E-03	6.40E-01	0.92	4.05	19q13
38	220011_at	MGC2603	1.39	9.77E-04	6.06E-01	0.83	4.03	1p35.3
39	224548_at	HES7	2.18	8.08E-04	6.06E-01	0.82	4.02	17p13.1
40	223648_s_at	FGFRL1	3.00	5.50E-04	6.06E-01	0.80	4.01	4p16
41	213306_at	MPDZ	2.64	5.86E-04	6.06E-01	0.81	4.01	9p24-p22
42	228583_at		1.82	6.54E-04	6.06E-01	0.80	3.99	

43	220833_at		2.63	7.16E-04	6.06E-01	0.81	3.99
44	209703_x_at	DKFZP586A0522	1.93	5.81E-04	6.06E-01	0.80	3.99 12q13.12
45	204337_at		2.37	6.75E-04	6.06E-01	0.79	3.93
46	215028_at	SEMA6A	3.58	7.15E-04	6.06E-01	0.79	3.92 5q23.1
47	211039_at	CHRNA1	2.55	8.87E-04	6.06E-01	0.79	3.92 2q24-q32
48	214668_at	C13orf1	2.88	8.41E-04	6.06E-01	0.81	3.92 13q14
49	206893_at	SALL1	3.75	9.27E-04	6.06E-01	0.79	3.91 16q12.1
50	209373_at	BENE	2.93	7.90E-04	6.06E-01	0.79	3.91 2q13

2.22 Status 2 versus normal

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	227935_s_at	MGC16202	-1.71	5.98E-07	2.21E-02	-0.66	-5.64	10q23.32
2	226196_s_at	MGC16028	2.29	1.00E-05	7.43E-02	0.74	5.42	14q24.2
3	204120_s_at	ADK	1.78	2.96E-05	9.11E-02	0.75	5.16	10cen-q24
4	200014_s_at - HG-U133B	HNRPC	1.30	2.33E-05	8.61E-02	0.66	5.01	14q11.1
5	218409_s_at	DNAJC1	1.65	2.88E-05	9.11E-02	0.64	4.91	10p12.31
6	205372_at	PLAG1	-3.49	6.16E-06	7.43E-02	-0.55	-4.87	8q12
7	220296_at	FLJ11715	-1.90	9.63E-06	7.43E-02	-0.54	-4.79	5q33.2
8	200021_at - HG-U133B	CFL1	-1.16	1.37E-05	7.43E-02	-0.55	-4.76	11q13
9	229963_at		-4.84	1.06E-05	7.43E-02	-0.53	-4.73	
10	230341_x_at	ADAMTS10	-1.74	1.41E-05	7.43E-02	-0.52	-4.64	19p13.2
11	203050_at	TP53BP1	1.64	1.29E-04	1.71E-01	0.70	4.62	15q15-q21
12	218643_s_at	CRIP1	1.82	9.19E-05	1.41E-01	0.63	4.60	2p21
13	212151_at		-2.68	1.84E-05	8.49E-02	-0.52	-4.59	
14	202972_s_at	FAM13A1	-1.40	2.23E-05	8.61E-02	-0.51	-4.53	4q22.1
15	208426_x_at	KIR2DL4	-1.43	3.48E-05	9.18E-02	-0.52	-4.50	19q13.4
16	214462_at	SOCS4	-1.57	5.36E-05	1.11E-01	-0.54	-4.47	18q22.2
17	224965_at	GNG2	-1.85	3.43E-05	9.18E-02	-0.50	-4.44	14q21
18	209014_at	MAGED1	1.80	2.50E-04	1.77E-01	0.71	4.41	Xp11.23
19	204044_at	QPRT	2.94	2.93E-04	1.89E-01	0.76	4.40	16p12.1
20	214290_s_at	HIST2H2AA	1.59	8.58E-05	1.38E-01	0.54	4.39	1q21.2
21	235463_s_at	LOC253782	1.61	1.76E-04	1.74E-01	0.61	4.39	2q31.1
22	232341_x_at	HABP4	-1.52	4.25E-05	9.80E-02	-0.50	-4.37	9q22.3-q31
23	204141_at	TUBB	-2.82	4.24E-05	9.80E-02	-0.49	-4.35	6p21.3
24	218829_s_at	KIAA1416	-1.91	5.41E-05	1.11E-01	-0.50	-4.33	8q12.1
25	202501_at	MAPRE2	1.57	1.94E-04	1.74E-01	0.59	4.32	18q12.1
26	200029_at - HG-U133B	RPL19	-1.13	7.79E-05	1.31E-01	-0.50	-4.27	17q11.2-q12
27	204197_s_at	RUNX3	-1.62	6.30E-05	1.22E-01	-0.48	-4.27	1p36
28	236248_x_at		-2.10	6.95E-05	1.28E-01	-0.48	-4.25	
29	201279_s_at	DAB2	1.80	1.71E-04	1.74E-01	0.53	4.21	5p13
30	200807_s_at	HSPD1	1.39	2.13E-04	1.74E-01	0.55	4.20	2q33.1
31	205070_at	ING3	-1.37	1.02E-04	1.50E-01	-0.49	-4.20	7q31
32	228003_at		-1.55	7.67E-05	1.31E-01	-0.47	-4.19	
33	203162_s_at	KATNB1	1.62	3.27E-04	1.89E-01	0.60	4.18	16q12.2

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34	205215_at	RNF2	1.51	1.57E-04	1.74E-01	0.51	4.17	1q25.2	
35	228011_at	LOC137392	3.49	5.24E-04	1.90E-01	0.72	4.15	8q21.3	
36	229971_at	GPR114	1.96	2.92E-04	1.89E-01	0.56	4.13	16q12.2	
37	203830_at	NJMU-R1	1.75	3.73E-04	1.89E-01	0.58	4.10	17q11.2	
38	213804_at	INPP5B	1.43	2.38E-04	1.77E-01	0.52	4.10	1p34	
39	227860_at	CPXM	2.43	5.11E-04	1.90E-01	0.63	4.08	20p12.3-p13	
40	222451_s_at	ZDHC9	1.95	3.72E-04	1.89E-01	0.56	4.08		9
41	229072_at		-2.52	1.10E-04	1.56E-01	-0.46	-4.08		
42	224617_at	ROD1	1.35	3.31E-04	1.89E-01	0.54	4.07	9q32	
43	235346_at	MGC51029	1.40	2.22E-04	1.74E-01	0.50	4.06	Xp11.3	
44	235556_at		-1.45	1.48E-04	1.74E-01	-0.46	-4.05		
45	210479_s_at	RORA	-2.18	1.30E-04	1.71E-01	-0.45	-4.03	15q21-q22	
46	218395_at	FLJ13433	1.60	4.50E-04	1.90E-01	0.56	4.01	12q23.2	
47	211296_x_at	UBC	-1.13	1.63E-04	1.74E-01	-0.46	-4.01	12q24.3	
48	202862_at	FAH	1.95	6.40E-04	1.91E-01	0.62	3.99	15q23-q25	
49	214697_s_at	ROD1	1.54	4.84E-04	1.90E-01	0.56	3.99	9q32	
50	224618_at	ROD1	1.58	4.28E-04	1.90E-01	0.54	3.99	9q32	

2.23 Status 3 versus Status 4

#	affy id	HUGO name	fc	p	q	strn	t	Map Location
1	36545_s_at	KIAA0542	-1.58	7.51E-07	4.75E-03	-1.49	-8.09	22q12.2
2	222753_s_at	FLJ22649	1.96	4.09E-08	1.51E-03	1.23	7.17	4q34.2
3	212608_s_at		-1.60	4.09E-05	3.52E-02	-1.36	-6.91	
4	221387_at	OT7T022	2.38	9.83E-08	1.82E-03	1.18	6.89	10q21-q22
5	239652_at		2.67	2.51E-07	2.32E-03	1.17	6.76	
6	227227_at		-1.84	2.44E-05	3.20E-02	-1.27	-6.69	
7	216117_at		2.99	2.29E-07	2.32E-03	1.16	6.63	
8	238109_at		-1.91	7.71E-07	4.75E-03	-1.10	-6.35	
9	45297_at	MGC45806	-3.80	1.08E-03	1.25E-01	-1.50	-6.24	1p35.2
10	219251_s_at	FLJ10300	-1.89	2.92E-06	1.08E-02	-1.10	-6.23	7q36.3
11	228331_at	SELH	-1.79	1.14E-05	2.18E-02	-1.12	-6.18	
12	244712_at		-2.45	2.35E-04	6.63E-02	-1.26	-6.14	
13	225180_at	FLJ00166	-1.89	2.74E-04	7.14E-02	-1.25	-6.08	3q27.2
14	219595_at	ZNF26	-1.33	1.16E-06	6.15E-03	-1.04	-6.01	12q24.33
15	229923_at		-1.52	3.25E-04	7.56E-02	-1.20	-5.86	
16	238346_s_at	NCOA6IP	1.58	1.92E-06	8.47E-03	1.00	5.83	8q11
17	230591_at		3.74	2.06E-06	8.47E-03	1.00	5.81	
18	206607_at	CBL	1.98	8.65E-06	1.98E-02	1.03	5.80	11q23.3
19	217526_at		-1.48	8.16E-05	4.84E-02	-1.08	-5.73	
20	220341_s_at	LOC51149	-1.89	3.87E-05	3.49E-02	-1.05	-5.72	5q35.3
21	220390_at	FLJ23598	-1.65	1.44E-04	5.86E-02	-1.09	-5.67	11p11.12
22	213851_at		2.38	3.81E-06	1.19E-02	0.97	5.66	
23	221686_s_at	RECQL5	-1.76	1.15E-04	5.33E-02	-1.08	-5.65	17q25.2-q25.3
24	207707_s_at	SEC13L1	1.50	3.38E-05	3.21E-02	1.02	5.62	3p25-p24

25 219833_s_at	FLJ10466	-1.67	1.08E-04	5.32E-02	-1.06	-5.61 6p12.1
26 232901_at	LOC57038	3.15	3.86E-06	1.19E-02	0.96	5.58 6q16.1
27 201280_s_at	DAB2	-2.05	1.22E-03	1.31E-01	-1.25	-5.55 5p13
28 221942_s_at	GUCY1A3	-2.43	9.17E-05	5.14E-02	-1.04	-5.55 4q31.1- q31.2
29 226959_at		-2.72	1.42E-03	1.39E-01	-1.26	-5.53
30 243886_at		-2.01	6.14E-05	4.37E-02	-1.01	-5.51
31 242491_at	SMA5	-1.61	4.01E-04	8.47E-02	-1.11	-5.50 5q13
32 230589_at		-2.10	6.38E-05	4.38E-02	-1.00	-5.46
33 228817_at		-1.38	9.10E-06	1.98E-02	-0.94	-5.44
34 217323_at	HLA-DRB6	3.18	2.72E-05	3.20E-02	0.96	5.40 6p21.3
35 238106_at		2.77	7.09E-06	1.98E-02	0.92	5.37
36 231896_s_at	DENR	-1.42	3.38E-04	7.56E-02	-1.05	-5.33 12q24.31
37 202885_s_at	PPP2R1B	3.36	8.75E-06	1.98E-02	0.91	5.31 11q23
38 212221_x_at		-1.86	2.38E-03	1.73E-01	-1.28	-5.30
39 200084_at - HG-U133B	SMAP	-1.39	1.95E-04	6.20E-02	-1.01	-5.29 11p15.1
40 222244_s_at	FLJ20618	-1.36	1.00E-04	5.20E-02	-0.97	-5.28 22q12.2
41 204939_s_at	PLN	3.40	8.75E-06	1.98E-02	0.91	5.28 6q22.1
42 217346_at		1.68	1.07E-04	5.32E-02	0.98	5.28
43 236695_at		2.88	9.95E-06	2.05E-02	0.90	5.27
44 235195_at		-1.78	9.10E-04	1.13E-01	-1.11	-5.27
45 219964_at	ST7L	-1.78	2.71E-05	3.20E-02	-0.92	-5.24 1p13.1
46 238588_at		-1.77	1.76E-04	6.09E-02	-0.98	-5.23
47 223716_s_at	ZNF265	-1.64	6.12E-04	1.03E-01	-1.06	-5.23 1p31
48 201005_at	CD9	-2.62	6.10E-04	1.03E-01	-1.06	-5.22 12p13.3
49 220530_at		4.48	1.18E-05	2.18E-02	0.90	5.21
50 217239_x_at		5.80	1.53E-05	2.65E-02	0.94	5.21

2.24 Status 3 versus Status 5

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	243322_at		4.13	6.00E-07	2.19E-02	1.08	6.32	
2	222461_s_at	HERC2	2.96	3.60E-06	2.31E-02	1.03	5.96	15q13
3	238067_at	FLJ20298	16.08	1.93E-06	2.19E-02	1.06	5.95	Xq22.2
4	215732_s_at	DTX2	2.18	1.18E-05	4.81E-02	1.04	5.87	7q11.23
5	206294_at	HSD3B2	3.33	1.85E-06	2.19E-02	0.98	5.78	1p13.1
6	215323_at		2.64	1.95E-06	2.19E-02	0.97	5.76	
7	208801_at	SRP72	-1.16	2.71E-06	2.31E-02	-0.96	-5.65	4q11
8	230982_at		3.38	2.27E-05	5.89E-02	1.01	5.63	
9	244854_at		3.35	3.70E-06	2.31E-02	0.94	5.57	
10	244858_at		3.24	4.52E-06	2.31E-02	0.94	5.52	
11	240691_at		4.46	4.62E-06	2.31E-02	0.94	5.50	
12	231010_at	PRO0971	1.64	7.35E-06	3.30E-02	0.94	5.49	4q25
13	218489_s_at	ALAD	-2.71	2.03E-04	1.55E-01	-1.07	-5.46	9q34
14	206936_x_at	NDUFC2	1.55	1.60E-05	5.59E-02	0.92	5.34	11q13.3
15	207834_at	FBLN1	2.65	1.62E-05	5.59E-02	0.89	5.21	22q13.31

16	229087_s_at	FLJ14775	2.52	7.87E-05	1.18E-01	0.93	5.17	17q25.1
17	219736_at	TRIM36	6.95	1.84E-05	5.89E-02	0.87	5.05	5q22.2
18	233395_at		1.46	2.46E-05	5.89E-02	0.86	5.03	
19	218121_at	HMOX2	1.76	1.87E-04	1.55E-01	0.93	5.01	16p13.3
20	244692_at	FLJ39501	3.69	2.30E-05	5.89E-02	0.85	5.00	19p13.11
21	203453_at	SCNN1A	2.77	2.09E-05	5.89E-02	0.85	4.99	12p13
22	214668_at	C13orf1	2.41	2.49E-05	5.89E-02	0.83	4.90	13q14
23	230987_at		2.09	1.88E-04	1.55E-01	0.89	4.88	
24	239849_at		3.52	5.30E-05	9.52E-02	0.84	4.86	
25	206159_at	GDF10	2.65	4.44E-05	8.46E-02	0.83	4.86	10q11.21
26	214408_s_at	RFPL3S	1.83	2.96E-04	1.85E-01	0.91	4.85	22q12.3
27	243155_at		3.36	3.43E-05	7.55E-02	0.82	4.80	
28	231073_at		2.35	3.53E-05	7.55E-02	0.81	4.78	
29	216651_s_at	GAD2	3.27	3.78E-04	2.17E-01	0.90	4.78	10p11.23
30	215270_at	LFNG	3.27	4.17E-05	8.46E-02	0.81	4.76	7p22
31	235187_s_at		2.74	4.52E-05	8.46E-02	0.79	4.70	
32	228950_s_at	FLJ23091	3.13	6.25E-05	1.04E-01	0.81	4.65	1p31.2
33	214893_x_at	HCN2	2.86	6.50E-05	1.04E-01	0.80	4.63	19p13.3
34	211132_at	FLJ21919	2.49	5.54E-05	9.57E-02	0.78	4.63	1q21.3
35	215802_at		3.33	1.05E-04	1.38E-01	0.79	4.59	
36	208314_at	RRH	1.57	1.97E-04	1.55E-01	0.81	4.58	4q25
37	238933_at	IRS1	3.02	7.72E-05	1.18E-01	0.80	4.58	2q36
38	243812_at	RABL4	2.14	1.94E-04	1.55E-01	0.81	4.56	22q13.1
39	230717_at		2.95	2.31E-04	1.62E-01	0.81	4.53	
40	241489_at		2.21	8.25E-04	2.76E-01	0.88	4.52	
41	243839_s_at		1.91	2.17E-04	1.60E-01	0.80	4.52	
42	234840_s_at	OR5V1	2.27	8.98E-05	1.30E-01	0.76	4.48	6p21.32
43	215028_at	SEMA6A	2.81	1.61E-04	1.50E-01	0.77	4.45	5q23.1
44	236870_at		2.94	9.50E-05	1.33E-01	0.75	4.44	
45	209373_at	BENE	3.04	1.83E-04	1.55E-01	0.77	4.43	2q13
46	204337_at		2.66	1.05E-04	1.38E-01	0.75	4.42	
47	243585_at		2.13	1.24E-04	1.39E-01	0.75	4.42	
48	207952_at	IL5	3.08	1.07E-04	1.38E-01	0.74	4.40	5q31.1
49	219793_at	SNX16	1.65	7.25E-04	2.63E-01	0.83	4.40	8q21.12
50	214823_at	ZNF204	1.84	1.27E-04	1.39E-01	0.75	4.39	6p21.3

2.25 Status 3 versus normal

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	214698_at	ROD1	1.95	8.94E-09	1.91E-04	0.84	7.08	9q32
2	214697_s_at	ROD1	1.66	2.12E-07	3.49E-04	0.70	6.04	9q32
3	203124_s_at	SLC11A2	-2.27	3.71E-08	2.44E-04	-0.64	-6.04	12q13
4	234863_x_at	FBXO5	-2.17	4.37E-08	2.44E-04	-0.63	-6.00	6q25-q26
5	217683_at		-3.37	4.55E-08	2.44E-04	-0.63	-5.99	
6	209458_x_at	HBA1	-1.80	1.03E-07	3.14E-04	-0.64	-5.90	16p13.3
7	211745_x_at	HBA2	-1.75	9.82E-08	3.14E-04	-0.63	-5.89	16p13.3

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8 237336_at	ADD2	-2.43	7.73E-08	3.14E-04	-0.62	-5.87 2p14-p13
9 211396_at	FCGR2B	-3.32	1.52E-07	3.46E-04	-0.66	-5.86 1q23
10 229610_at	FLJ40629	-2.15	1.24E-07	3.33E-04	-0.61	-5.78 2q13
11 211699_x_at	HBA1	-1.82	1.62E-07	3.46E-04	-0.61	-5.75 16p13.3
12 56748_at	TRIM10	-1.90	1.78E-07	3.47E-04	-0.61	-5.71 6p21.3
13 203891_s_at	DAPK3	1.75	4.53E-07	4.41E-04	0.64	5.69 19p13.3
14 218726_at	DKFZp762E1312	-2.59	2.64E-07	3.62E-04	-0.61	-5.66 2q37.1
15 206834_at	HBD	-2.44	1.95E-07	3.49E-04	-0.60	-5.65 11p15.5
16 203581_at	RAB4A	1.57	1.24E-06	7.20E-04	0.68	5.63 1q42-q43
17 221509_at	DENR	1.51	1.21E-06	7.20E-04	0.67	5.63 12q24.31
18 209301_at	CA2	-3.06	2.94E-07	3.64E-04	-0.60	-5.61 8q22
19 203214_x_at	CDC2	-2.11	3.06E-07	3.64E-04	-0.60	-5.59 10q21.1
20 206574_s_at	PTP4A3	4.97	4.56E-06	1.11E-03	0.84	5.59
21 227309_at		-2.04	2.70E-07	3.62E-04	-0.59	-5.59
22 204018_x_at	HBA1	-1.70	3.80E-07	4.07E-04	-0.60	-5.59 16p13.3
23 226944_at	HTRA3	-2.04	2.66E-07	3.62E-04	-0.59	-5.58 4p16.1
24 213800_at	HF1	4.91	4.54E-06	1.11E-03	0.81	5.56 1q32
25 202043_s_at	SMS	1.55	1.39E-06	7.27E-04	0.66	5.56 Xp22.1
26 231274_s_at	MSCP	-2.57	3.57E-07	4.03E-04	-0.60	-5.56 8p21.2
27 202701_at	BMP1	1.61	1.06E-06	7.09E-04	0.64	5.55 8p21
28 239327_at		-4.20	5.37E-07	5.00E-04	-0.61	-5.52
29 207252_at	INE1	-2.14	4.15E-07	4.23E-04	-0.58	-5.48 Xp11.4-p11.3
30 74694_s_at	FRA	1.57	2.49E-06	8.90E-04	0.65	5.44 16p12.1
31 205592_at	SLC4A1	-5.93	7.78E-07	6.44E-04	-0.60	-5.43 17q21-q22
32 214414_x_at	HBA1	-1.50	8.84E-07	7.01E-04	-0.59	-5.40 16p13.3
33 209392_at	ENPP2	4.70	8.31E-06	1.37E-03	0.80	5.37 8q24.1
34 217010_s_at	CDC25C	-1.99	7.81E-07	6.44E-04	-0.57	-5.37 5q31
35 208416_s_at	SPTB	-7.29	1.08E-06	7.09E-04	-0.60	-5.36 14q23-q24.2
36 203123_s_at	SLC11A2	-1.59	7.06E-07	6.30E-04	-0.56	-5.34 12q13
37 217232_x_at	HBB	-1.59	1.53E-06	7.79E-04	-0.59	-5.33 11p15.5
38 224587_at	PC4	1.51	3.07E-06	9.54E-04	0.62	5.31 5p13.3
39 204419_x_at	HBG2	-2.94	9.58E-07	7.09E-04	-0.56	-5.27 11p15.5
40 210559_s_at	CDC2	-2.23	1.12E-06	7.09E-04	-0.56	-5.27 10q21.1
41 210384_at	HRMT1L1	-2.28	1.01E-06	7.09E-04	-0.55	-5.26 21q22.3
42 209116_x_at	HBB	-1.63	2.02E-06	8.53E-04	-0.58	-5.26 11p15.5
43 213515_x_at	HBG1	-2.82	1.03E-06	7.09E-04	-0.55	-5.25 11p15.5
44 220886_at	GABRQ	-1.48	1.17E-06	7.17E-04	-0.55	-5.24 Xq28
45 205678_at	AP3B2	-1.72	1.12E-06	7.09E-04	-0.55	-5.23 15q
46 218188_s_at	TIMM13	1.81	8.01E-06	1.37E-03	0.67	5.21 19p13.3
47 211819_s_at	SORBS1	-1.69	1.34E-06	7.23E-04	-0.55	-5.20 10q23.3-q24.1
48 215150_at	PRO0907	-1.67	1.32E-06	7.23E-04	-0.55	-5.19 1q32.1
49 234742_at	SIRPB2	-2.20	1.35E-06	7.23E-04	-0.55	-5.19 20p13
50 203897_at	LOC57149	2.01	1.17E-05	1.73E-03	0.72	5.18 16p11.2

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	206936_x_at	NDUFC2	1.92	3.20E-05	8.13E-01	2.70	8.76	11q13.3
2	201005_at	CD9	8.14	1.94E-04	8.27E-01	2.62	8.11	12p13.3
3	223848_at		3.11	5.45E-05	8.13E-01	2.47	7.98	
4	218489_s_at	ALAD	-4.76	1.18E-04	8.27E-01	-2.37	-7.55	9q34
5	203950_s_at	CLCN6	1.88	6.16E-05	8.13E-01	2.19	7.21	1p36
6	243866_x_at		3.19	1.09E-04	8.27E-01	2.13	6.99	
7	205081_at	CRIP1	3.05	1.30E-04	8.27E-01	1.99	6.56	7q11.23
8	39248_at	AQP3	4.84	1.08E-03	8.27E-01	2.09	6.30	9p13
9	208978_at	CRIP2	17.82	3.61E-03	8.27E-01	2.48	6.04	14q32.3
10	224619_at	LOC113201	2.30	6.24E-04	8.27E-01	1.86	5.94	15q14
11	210757_x_at	DAB2	2.40	5.46E-04	8.27E-01	1.83	5.88	5p13
12	45297_at	MGC45806	4.48	5.02E-04	8.27E-01	1.80	5.84	1p35.2
13	206574_s_at	PTP4A3	5.86	1.30E-03	8.27E-01	1.86	5.73	
14	230601_s_at	MGC16309	1.74	3.11E-04	8.27E-01	1.73	5.72	17q21.32
15	228817_at		1.57	8.27E-04	8.27E-01	1.80	5.67	
16	231100_at	RRAD	-2.43	4.09E-04	8.27E-01	-1.71	-5.62	16q22
17	230434_at	MGC22679	1.83	8.84E-04	8.27E-01	1.75	5.58	2q31.1
18	201494_at	PRCP	1.63	4.90E-04	8.27E-01	1.69	5.56	11q14
19	237240_at		1.74	6.01E-04	8.27E-01	1.71	5.54	
20	204073_s_at	C11orf9	3.07	4.04E-04	8.27E-01	1.66	5.50	11q12-q13.1
21	202111_at	SLC4A2	4.55	1.84E-03	8.27E-01	1.79	5.47	7q35-q36
22	209373_at	BENE	4.40	1.58E-03	8.27E-01	1.75	5.44	2q13
23	208120_x_at		1.68	2.88E-03	8.27E-01	1.83	5.38	
24	206204_at	GRB14	6.16	5.28E-03	8.27E-01	2.11	5.36	2q22-q24
25	211856_x_at	CD28	3.41	2.71E-03	8.27E-01	1.80	5.35	2q33
26	202944_at	NAGA	2.06	1.53E-03	8.27E-01	1.70	5.33	22q13-qter
27	217526_at		1.58	5.18E-04	8.27E-01	1.61	5.32	
28	240321_at		2.73	2.51E-03	8.27E-01	1.85	5.28	
29	204446_s_at	ALOX5	3.79	1.12E-03	8.27E-01	1.64	5.27	10q11.2
30	213317_at		2.31	5.40E-04	8.27E-01	1.58	5.24	
31	210123_s_at	CHRNA7	1.98	9.00E-04	8.27E-01	1.60	5.20	15q14
32	223637_s_at	DKFZP566M1046	1.44	3.18E-03	8.27E-01	1.72	5.13	11p15.4
33	221659_s_at	LOC93408	-1.75	3.27E-03	8.27E-01	-1.80	-5.06	7q22.1
34	227032_at	FLJ30634	2.28	8.60E-04	8.27E-01	1.54	5.05	1q32.1
35	212921_at	HSKM-B	1.69	8.14E-04	8.27E-01	1.54	5.05	1q32.3
36	222138_s_at	WDR13	1.99	8.81E-04	8.27E-01	1.51	4.99	Xp11.23
37	222976_s_at	TPM3	1.22	1.03E-03	8.27E-01	1.52	4.97	1q21.2
38	235087_at	UNKL	-6.35	3.70E-03	8.27E-01	-1.78	-4.95	16p13.3
39	209561_at	THBS3	1.93	2.93E-03	8.27E-01	1.61	4.93	1q21
40	201280_s_at	DAB2	2.49	8.15E-04	8.27E-01	1.49	4.93	5p13
41	205160_at	PEX11A	1.96	1.08E-03	8.27E-01	1.50	4.93	15q25.3
42	200811_at	CIRBP	1.49	8.54E-04	8.27E-01	1.48	4.90	19p13.3
43	209695_at	PTP4A3	2.45	1.19E-03	8.27E-01	1.49	4.88	
44	220974_x_at	BA108L7.2	2.36	9.31E-04	8.27E-01	1.47	4.88	10q24.31
45	201430_s_at	DPYSL3	3.30	3.56E-03	8.27E-01	1.61	4.88	5q32

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46 229458_s_at	GALK1	2.23	3.31E-03	8.27E-01	1.59	4.85 17q24
47 211289_x_at	CDC2L2	1.77	1.42E-03	8.27E-01	1.48	4.82 1p36.3
48 238382_x_at		1.75	1.10E-03	8.27E-01	1.46	4.81
49 200862_at	DHCR24	3.77	7.22E-03	8.27E-01	1.81	4.80 1p33-p31.1
50 222249_at		3.15	2.17E-03	8.27E-01	1.51	4.80

2.27 Status 4 versus normal

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	202371_at	FLJ21174	2.24	1.23E-08	3.35E-06	1.88	12.92	Xq22.1
2	219251_s_at	FLJ10300	3.11	1.11E-06	8.15E-05	2.04	12.64	7q36.3
3	201242_s_at	ATP1B1	2.84	2.98E-09	1.44E-06	1.68	11.97	1q22-q25
4	201022_s_at	DSTN	1.85	1.15E-07	1.66E-05	1.76	11.81	20p11.23
5	201536_at	DUSP3	1.87	1.84E-15	4.61E-11	1.36	10.96	17q21
6	220761_s_at	JK	1.78	4.99E-11	1.13E-07	1.42	10.76	12q
7	222753_s_at	FLJ22649	-2.14	2.51E-13	2.09E-09	-1.33	-10.51	4q34.2
8	203227_s_at	SAS	2.54	2.50E-05	7.09E-04	1.82	10.33	12q13.3
9	221005_s_at	PTDSS2	2.29	6.36E-07	5.49E-05	1.51	10.10	11p15
10	231896_s_at	DENR	1.94	5.41E-05	1.23E-03	1.84	9.96	12q24.31
11	221509_at	DENR	1.98	6.13E-05	1.35E-03	1.86	9.95	12q24.31
12	221942_s_at	GUCY1A3	5.10	1.85E-04	2.98E-03	2.15	9.93	4q31.1-q31.2
13	238109_at		2.67	3.10E-10	4.08E-07	1.26	9.64	
14	216117_at		-3.38	4.80E-14	6.00E-10	-1.18	-9.62	
15	210425_x_at	GOLGIN-67	3.51	2.06E-04	3.24E-03	1.97	9.39	15q11.2
16	212608_s_at		1.83	4.51E-05	1.08E-03	1.64	9.34	
17	36545_s_at	KIAA0542	1.74	4.97E-08	9.93E-06	1.28	9.24	22q12.2
18	204756_at	MAP2K5	1.87	3.62E-06	1.88E-04	1.40	9.14	15q22.2
19	219833_s_at	FLJ10466	2.21	5.50E-05	1.24E-03	1.60	9.10	6p12.1
20	203807_x_at	CSH2	-2.13	7.84E-11	1.51E-07	-1.15	-9.00	17q24.2
21	214344_at	LOC92973	-6.45	7.05E-13	4.41E-09	-1.12	-9.00	9p13.1
22	220044_x_at	LUC7A	2.05	3.52E-05	9.04E-04	1.51	8.92	17q21
23	200631_s_at	SET	1.38	5.23E-06	2.38E-04	1.36	8.87	9q34
24	211727_s_at	COX11	2.28	3.29E-04	4.51E-03	1.90	8.79	17q22
25	219964_at	ST7L	2.36	8.73E-07	6.78E-05	1.27	8.77	1p13.1
26	220341_s_at	LOC51149	2.52	1.30E-05	4.62E-04	1.38	8.74	5q35.3
27	218983_at	LOC51279	2.78	2.96E-04	4.19E-03	1.80	8.64	12p13.31
28	200084_at - HG-U133B	SMAP	1.64	4.52E-05	1.08E-03	1.43	8.53	11p15.1
29	221671_x_at	IGKC	-6.22	5.10E-12	2.12E-08	-1.05	-8.51	2p12
30	216656_at		-1.76	4.43E-12	2.12E-08	-1.05	-8.50	
31	225178_at	FLJ00166	2.16	9.53E-08	1.49E-05	1.16	8.48	3q27.2
32	221651_x_at	IGKC	-5.79	1.11E-11	3.97E-08	-1.05	-8.45	2p12
33	227227_at		2.15	8.62E-06	3.38E-04	1.27	8.30	
34	242810_x_at		-5.26	2.72E-11	6.80E-08	-1.02	-8.26	
35	215943_at	KIAA1661	-4.50	1.28E-11	3.98E-08	-1.01	-8.24	
36	214677_x_at	IGLJ3	-8.00	1.49E-11	4.13E-08	-1.01	-8.19	22q11.1-q11.2

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37	225180_at	FLJ00166	2.37	2.17E-04	3.37E-03	1.55	8.17 3q27.2
38	204909_at	DDX6	-1.78	9.30E-10	8.61E-07	-1.03	-8.08 11q23.3
39	213359_at		1.53	1.47E-07	2.03E-05	1.09	8.04
40	217157_x_at	IGKC	-5.81	7.60E-11	1.51E-07	-1.00	-8.02 2p12
41	211302_s_at	PDE4B	-3.40	1.24E-10	2.20E-07	-1.00	-7.99 1p31
42	214698_at	ROD1	2.00	9.75E-05	1.88E-03	1.38	7.99 9q32
43	205896_at	SLC22A4	-3.04	2.18E-09	1.24E-06	-1.02	-7.96 5q31.1
44	201280_s_at	DAB2	3.14	6.44E-04	7.29E-03	1.81	7.95 5p13
45	225227_at		-4.18	1.32E-10	2.20E-07	-0.97	-7.84
46	235391_at	LOC137392	3.14	5.07E-04	6.13E-03	1.66	7.83 8q21.3
47	215733_x_at	CTAG2	-1.84	1.66E-10	2.60E-07	-0.96	-7.76 Xq28
48	204341_at	TRIM16	2.83	9.76E-04	9.86E-03	1.98	7.75 17p11.2
49	204073_s_at	C11orf9	3.35	7.97E-04	8.57E-03	1.79	7.69 11q12-q13.1
50	221765_at	UGCG	-4.38	5.48E-09	1.96E-06	-0.99	-7.69 9q31

2.28 Status 5 versus normal

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	219065_s_at	CGI-27	1.41	7.97E-14	2.39E-09	1.23	9.92	2p23.1
2	243322_at		-4.34	2.21E-08	3.91E-05	-1.24	-9.04	
3	207052_at	HAVCR1	-3.03	8.85E-08	7.81E-05	-1.22	-8.78	5q33.2
4	206159_at	GDF10	-3.59	4.49E-09	1.13E-05	-1.07	-8.21	10q11.21
5	226464_at	MGC33365	-2.42	3.02E-09	1.01E-05	-1.05	-8.14	3q24
6	203673_at	TG	-2.52	2.39E-07	1.46E-04	-1.11	-8.01	8q24.2-q24.3
7	243010_at	MSI2	1.88	3.87E-07	1.90E-04	1.10	7.87	17q23.1
8	204337_at		-3.50	1.81E-09	7.76E-06	-0.96	-7.64	
9	220542_s_at	PLUNC	-2.37	3.57E-08	4.75E-05	-0.97	-7.45	20q11.2
10	229894_s_at	KIAA1160	-1.94	1.10E-09	7.76E-06	-0.89	-7.26	3q21.3
11	208007_at		-3.82	1.07E-09	7.76E-06	-0.89	-7.24	
12	205879_x_at	RET	-2.16	2.14E-08	3.91E-05	-0.92	-7.20	10q11.2
13	208801_at	SRP72	1.22	1.63E-09	7.76E-06	0.87	7.09	4q11
14	214668_at	C13orf1	-2.98	2.87E-09	1.01E-05	-0.88	-7.08	13q14
15	214981_at		-6.47	1.44E-09	7.76E-06	-0.86	-7.05	
16	216661_x_at	CYP2C9	-1.93	1.53E-09	7.76E-06	-0.86	-7.05	10q24
17	244692_at	FLJ39501	-5.04	5.81E-09	1.24E-05	-0.88	-7.04	19p13.11
18	226140_s_at		-2.67	1.03E-07	8.31E-05	-0.91	-6.98	
19	204687_at	DKFZP564O0823	-1.75	1.27E-07	9.53E-05	-0.91	-6.97	4q13.3-q21.3
20	202008_s_at	NID	-2.60	4.54E-09	1.13E-05	-0.86	-6.95	1q43
21	239286_at		-3.91	3.51E-07	1.83E-04	-0.91	-6.89	
22	219504_s_at	FLJ13150	1.92	3.54E-07	1.83E-04	0.91	6.88	1p22.1
23	231380_at	VEST1	-5.03	3.41E-09	1.02E-05	-0.84	-6.85	8q13
24	201074_at	SMARCC1	1.34	8.59E-08	7.81E-05	0.87	6.80	3p23-p21
25	231981_at		-2.24	5.97E-08	6.92E-05	-0.87	-6.79	
26	206204_at	GRB14	-5.37	4.97E-09	1.15E-05	-0.83	-6.76	2q22-q24
27	209535_s_at	AKAP13	-2.15	1.27E-06	3.52E-04	-0.92	-6.75	15q24-q25

28 201664_at	SMC4L1	1.71	5.72E-05	3.71E-03	1.06	6.69 3q26.1
29 221370_at	ZNF73	-2.98	3.25E-06	6.45E-04	-0.93	-6.67 22p
30 233836_at		-2.84	8.63E-09	1.73E-05	-0.81	-6.62
31 227948_at	FRABIN	-3.00	2.43E-07	1.46E-04	-0.85	-6.58 12p11.1
32 241821_at		-2.29	2.49E-07	1.46E-04	-0.85	-6.57
33 223750_s_at	TLR10	-3.30	8.34E-08	7.81E-05	-0.82	-6.51 4p14
34 216231_s_at	B2M	-1.17	7.42E-08	7.68E-05	-0.82	-6.49 15q21-q22.2
35 239567_at		-3.85	2.15E-07	1.42E-04	-0.82	-6.44
36 230982_at		-3.68	3.26E-06	6.45E-04	-0.88	-6.43
37 206294_at	HSD3B2	-2.83	1.38E-07	1.01E-04	-0.81	-6.41 1p13.1
38 215086_at	IBTK	-7.05	2.72E-08	4.30E-05	-0.78	-6.34 6q14.3
39 210115_at	RPL39L	-5.24	2.55E-08	4.26E-05	-0.77	-6.33 3q27
40 231073_at		-2.64	3.64E-08	4.75E-05	-0.78	-6.33
41 240016_at		-2.83	3.45E-07	1.83E-04	-0.81	-6.32
42 244854_at		-4.22	3.49E-08	4.75E-05	-0.77	-6.30
43 206843_at	CRYBA4	-2.86	1.12E-07	8.62E-05	-0.79	-6.30 22q12.1
44 207952_at	IL5	-3.52	7.68E-08	7.68E-05	-0.78	-6.26 5q31.1
45 243132_at		-3.52	3.59E-08	4.75E-05	-0.77	-6.26
46 204762_s_at	GNAO1	-1.81	2.64E-07	1.49E-04	-0.79	-6.25 16q13
47 209948_at	KCNMB1	-1.80	2.45E-06	5.45E-04	-0.83	-6.23 5q34
48 208812_x_at	HLA-C	-1.21	1.05E-07	8.31E-05	-0.78	-6.23 6p21.3
49 218329_at	PRDM4	-1.67	1.04E-07	8.31E-05	-0.77	-6.22 12q23-q24.1
50 41397_at	LOC55565	-2.90	4.74E-07	2.05E-04	-0.80	-6.21 16q22.1

Claims

1. A method for distinguishing AML-specific FLT3 length mutations from TKD mutations in a sample, the method comprising determining the expression level of markers selected from the markers identifiable by their Affymetrix Identification Numbers (affy ID) as defined in Tables 1, and/or 2,

wherein

- a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.1 having a negative fc value, and/or a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.1 having a positive fc value, is indicative for the presence of AML_D835 when AML_D835 is distinguished from all other subtypes,

and/or wherein

- a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.2 having a negative fc value, and/or a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.2 having a positive fc value, is indicative for the presence of AML_Double when AML_Double is distinguished from all other subtypes,

and/or wherein

- a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.3 having a negative fc value, and/or a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.3 having a positive fc value, is indicative for the presence of AML_Status-1 when AML_Status-1 is distinguished from all other subtypes,

and/or wherein

- a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.4 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.4 having a positive fc value,
is indicative for the presence of AML_Status-2 when AML_Status-2 is distinguished from all other subtypes,

5 and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.5 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.5 having a positive fc value,

10 is indicative for the presence of AML_Status-3 when AML_Status-3 is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.6 having a negative fc value, and/or

15 a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.6 having a positive fc value,
is indicative for the presence of AML_Status-4 when AML_Status-4 is distinguished from all other subtypes,

and/or wherein

20 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.7 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.7 having a positive fc value,

25 is indicative for the presence of AML_Status-5 when AML_Status-5 is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.8 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.8 having a positive fc value,

30

is indicative for the presence of AML_normal when AML_normal is distinguished from all other subtypes,

and/or wherein

5 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.1 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.1 having a positive fc value,

is indicative for the presence of AML_D835 when AML_D835 is distinguished from AML_Double,

10 and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.2 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.2 having a positive fc value,

15 is indicative for the presence of AML_D835 when AML_D835 is distinguished from AML_Status-1,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.3 having a negative fc value, and/or

20 a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.3 having a positive fc value,

is indicative for the presence of AML_D835 when AML_D835 is distinguished from AML_Status-2,

and/or wherein

25 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.4 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.4 having a positive fc value,

30 is indicative for the presence of AML_D835 when AML_D835 is distinguished from AML_Status-3,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.5 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.5 having a positive fc value,
5 is indicative for the presence of AML_D835 when AML_D835 is distinguished from AML_Status-4,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.6 having a negative fc value, and/or
10 a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.6 having a positive fc value,
is indicative for the presence of AML_D835 when AML_D835 is distinguished from AML_Status-5,

and/or wherein

15 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.7 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.7 having a positive fc value,
is indicative for the presence of AML_D835 when AML_D835 is
20 distinguished from AML_normal,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.8 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least
25 one of the numbers 1 to 50 of Table 2.8 having a positive fc value,
is indicative for the presence of AML_Double when AML_Double is distinguished from AML_Status-1,

and/or wherein

30 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.9 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.9 having a positive fc value,
is indicative for the presence of AML_Double when AML_Double is distinguished from AML_Status-2,

5 and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.10 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.10 having a positive fc value,
10 is indicative for the presence of AML_Double when AML_Double is distinguished from AML_Status-3,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.11 having a negative fc value, and/or
15 a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.11 having a positive fc value,
is indicative for the presence of AML_Double when AML_Double is distinguished from AML_Status-4,

and/or wherein

20 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.12 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.12 having a positive fc value,
is indicative for the presence of AML_Double when AML_Double is distinguished from AML_Status-5,
25

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.13 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.13 having a positive fc value,
30

is indicative for the presence of AML_Double when AML_Double is distinguished from AML_normal,

and/or wherein

5 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.14 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.14 having a positive fc value,
is indicative for the presence of AML_Status-1 when AML_Status-1 is distinguished from AML_Status-2,

10 and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.15 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.15 having a positive fc value,
15 is indicative for the presence of AML_Status-1 when AML_Status-1 is distinguished from AML_Status-3,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.16 having a negative fc value, and/or
20 a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.16 having a positive fc value,
is indicative for the presence of AML_Status-1 when AML_Status-1 is distinguished from AML_Status-4,

and/or wherein

25 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.17 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.17 having a positive fc value,
is indicative for the presence of AML_Status-1 when AML_Status-1 is distinguished from AML_Status-5,
30

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.18 having a negative fc value, and/or a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.18 having a positive fc value,
5 is indicative for the presence of AML_Status-1 when AML_Status-1 is distinguished from AML_normal,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.19 having a negative fc value, and/or
10 a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.19 having a positive fc value,
is indicative for the presence of AML_Status-2 when AML_Status-2 is distinguished from AML_Status-3,

and/or wherein

15 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.20 having a negative fc value, and/or a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.20 having a positive fc value,
is indicative for the presence of AML_Status-2 when AML_Status-2 is
20 distinguished from AML_Status-4,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.21 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least
25 one of the numbers 1 to 50 of Table 2.21 having a positive fc value,
is indicative for the presence of AML_Status-2 when AML_Status-2 is distinguished from AML_Status-5,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one
30 of the numbers 1 to 50 of Table 2.22 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.22 having a positive fc value,
is indicative for the presence of AML_Status-2 when AML_Status-2 is distinguished from AML_normal,

5 and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.23 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.23 having a positive fc value,
10 is indicative for the presence of AML_Status-3 when AML_Status-3 is distinguished from AML_Status-4,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.24 having a negative fc value, and/or
15 a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.24 having a positive fc value,
is indicative for the presence of AML_Status-3 when AML_Status-3 is distinguished from AML_Status-5,

and/or wherein

20 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.25 having a negative fc value, and/or
a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.25 having a positive fc value,
is indicative for the presence of AML_Status-3 when AML_Status-3 is distinguished from AML_normal,
25

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.26 having a negative fc value, and/or
30 a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.26 having a positive fc value,

is indicative for the presence of AML_Status-4 when AML_Status-4 is distinguished from AML_Status-5,

and/or wherein

5 a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.27 having a negative fc value, and/or a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.27 having a positive fc value, is indicative for the presence of AML_Status-4 when AML_Status-4 is distinguished from AML_normal,

10 and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.28 having a negative fc value, and/or a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.28 having a positive fc value, 15 is indicative for the presence of AML_Status-5 when AML_Status-5 is distinguished from AML_normal.

2. The method according to claim 1 wherein the polynucleotide is labelled.

20 3. The method according to claim 1 or 2, wherein the label is a luminescent, preferably a fluorescent label, an enzymatic or a radioactive label.

4. The method according at least one of the claims 1-3, wherein the expression level of at least two, preferably of at least ten, more preferably of at least 25, most preferably of 50 of the markers of at least one of the Tables 1-2 is 25 determined.

5. The method according to at least one of the claims 1-4, wherein the expression level of markers expressed lower in a first subtype than in at least one second subtype, which differs from the first subtype, is at least 5 30

%, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold lower, preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold lower in the first subtype.

- 5 6. The method according to at least one of the claims 1-4, wherein the expression level of markers expressed higher in a first subtype than in at least one second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold higher, preferably at least 10-fold, more preferably at least 50-
10 fold, and most preferably at least 100-fold higher in the first subtype.
7. The method according to at least one of the claims 1-6, wherein the sample is from an individual having AML.
- 15 8. The method according to at least one of the claims 1-7, wherein at least one polynucleotide is in the form of a transcribed polynucleotide, or a portion thereof.
- 20 9. The method according to claim 8, wherein the transcribed polynucleotide is a mRNA or a cDNA.
- 25 10. The method according to claim 8 or 9, wherein the determining of the expression level comprises hybridizing the transcribed polynucleotide to a complementary polynucleotide, or a portion thereof, under stringent hybridization conditions.
11. The method according to at least one of the claims 1-7, wherein at least one polynucleotide is in the form of a polypeptide, or a portion thereof.

12. The method according to at least one of the claims 8, 9 or 12, wherein the determining of the expression level comprises contacting the polynucleotide or the polypeptide with a compound specifically binding to the polynucleotide or the polypeptide.
- 5
13. The method according to claim 12, wherein the compound is an antibody, or a fragment thereof.
14. The method according to at least one of the claims 1-13, wherein the method is carried out on an array.
- 10
15. The method according to at least one of the claims 1-14, wherein the method is carried out in a robotics system.
- 15
16. The method according to at least one of the claims 1-15, wherein the method is carried out using microfluidics.
17. Use of at least one marker as defined in at least one of the claims 1-3 for the manufacturing of a diagnostic for distinguishing AML-specific FLT3 length mutations from TKD mutations.
- 20
18. The use according to claim 17 for distinguishing AML_MLL, t(15;17), t(8;21), inv(16), 11q23, de novo_AML, s_AML, t_AML, AML_M0, AML_M1, AML_M2, AML_M4, AML_M5a, AML_M5b, AML_M6, AML_t(15;17)/M3 and/or AML_t(15;17)/M3v in an individual having AML.
- 25
19. A diagnostic kit containing at least one marker as defined in at least one of the claims 1-3 for distinguishing AML-specific FLT3 length mutations from TKD mutations, in combination with suitable auxiliaries.
- 30

20. The diagnostic kit according to claim 19, wherein the kit contains at least one reference for the AML-specific FLT3 length mutations and/or TKD mutations.
- 5
21. The diagnostic kit according to claim 20, wherein the reference is a sample or a data bank.
22. An apparatus for distinguishing AML-specific FLT3 length mutations from TKD mutations in a sample containing a reference data bank.
- 10
23. The apparatus according to claim 22, wherein the reference data bank is obtainable by comprising
- 15
- (a) compiling a gene expression profile of a patient sample by determining the expression level of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy ID) as defined in Tables 1, and/or 2, and
- (b) classifying the gene expression profile by means of a machine learning algorithm.
- 20
24. The apparatus according to claim 23, wherein the machine learning algorithm is selected from the group consisting of Weighted Voting, K-Nearest Neighbors, Decision Tree Induction, Support Vector Machines, and Feed-Forward Neural Networks, preferably Support Vector Machines.
- 25
25. The apparatus according to at least one of the claims 22-24, wherein the apparatus contains a control panel and/or a monitor.
26. A reference data bank for distinguishing AML-specific FLT3 length mutations from TKD mutations obtainable by comprising
- 30
- (a) compiling a gene expression profile of a patient sample by determining the expression level of at least one marker selected

from the markers identifiable by their Affymetrix Identification Numbers (affy ID) as defined in Tables 1, and/or 2, and

(b) classifying the gene expression profile by means of a machine learning algorithm.

5

27. The reference data bank according to claim 26, wherein the reference data bank is backed up and/or contained in a computational memory chip.

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
12 May 2005 (12.05.2005)

PCT

(10) International Publication Number
WO 2005/043168 A3

- (51) International Patent Classification⁷: G01N 33/574, C12Q 1/68
- (74) Common Representative: ROCHE DIAGNOSTICS GMBH; Burger Alexander, Patent Department (TR-E), Postfach 11 52, 82372 Penzberg (DE).
- (21) International Application Number: PCT/EP2004/012470
- (81) Designated States (*unless otherwise indicated, for every kind of national protection available*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.
- (22) International Filing Date: 4 November 2004 (04.11.2004)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data: 03025341.3 4 November 2003 (04.11.2003) EP
- (84) Designated States (*unless otherwise indicated, for every kind of regional protection available*): ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).
- (71) Applicant (*for DE only*): ROCHE DIAGNOSTICS GMBH [DE/DE]; Sandhofer Strasse 116, 68305 Mannheim (DE).
- (71) Applicant (*for all designated States except DE, US*): F. HOFFMANN-LA ROCHE AG [CH/CH]; Grenzacherstrasse 124, CH-4070 Basel (CH).
- (72) Inventors; and
- (75) Inventors/Applicants (*for US only*): HAFFERLACH, Torsten [DE/DE]; Springerstrasse 8, 81477 Muenchen (DE). DUGAS, Martin [DE/DE]; Michael-Fischer-Platz 6, 94469 Deggendorf (DE). KERN, Wolfgang [DE/DE]; Hanfelder Strasse 101, 82319 Starnberg (DE). KOHLMANN, Alexander [DE/DE]; Schwarzstrasse 14, 92318 Neumarkt (DE). SCHNITTGER, Susanne [DE/DE]; Saalburgstrasse 2a, 81375 Muenchen (DE). SCHOCH, Claudia [DE/DE]; Springerstrasse 8, 81477 Muenchen (DE).
- Published:
- with international search report
 - before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments
- (88) Date of publication of the international search report: 11 August 2005
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

WO 2005/043168 A3

(54) Title: METHOD FOR DISTINGUISHING AML-SPECIFIC FLT3 LENGTH MUTATIONS FROM TKD MUTATIONS

(57) Abstract: Disclosed is a method for distinguishing AML-specific FLT3 length mutations from TKD mutations in a sample by determining the expression level of markers, as well as a diagnostic kit and an apparatus containing the markers.

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP2004/012470

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 G01N33/574 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 G01N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, WPI Data, EMBASE, MEDLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	<p>DATABASE BIOSIS 'Online! BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2002 (2002-11-16), SCHNITTGER SUSANNE ET AL: "Acute Myeloid Leukemia (AML) with FLT3-Length Mutations (FLT3-LM) Can Be Discriminated from AML without FLT3-LM in Distinct AML-Subtypes Based on Specific Gene Expression Profiles." XP002272702 Database accession no. PREV200300335803 abstract</p> <p style="text-align: center;">-/-</p>	1-27

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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Date of the actual completion of the international search

2 March 2005

Date of mailing of the international search report

24. 06. 2005

Name and mailing address of the ISA

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP2004/012470

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	<p>& BLOOD, vol. 100, no. 11, 16 November 2002 (2002-11-16), page Abstract No. 1203, 44th Annual Meeting of the American Society of Hematology; Philadelphia, PA, USA; December 06-10, 2002 ISSN: 0006-4971</p> <hr/> <p>DATABASE BIOSIS 'Online! BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2001 (2001-11-16), NIGRO CRISTIANA LO ET AL: "Internal tandem duplication and D385 mutation analysis of Flt3 gene in AML patients" XP002272703 Database accession no. PREV200200152170 abstract & BLOOD, vol. 98, no. 11 Part 2, 16 November 2001 (2001-11-16), page 190b, 43rd Annual Meeting of the American Society of Hematology, Part 2; Orlando, Florida, USA; December 07-11, 2001 ISSN: 0006-4971</p>	1-27
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INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP2004/012470

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	<p>DATABASE BIOSIS 'Online! BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2002 (2002-11-16), SCHNITTGER SUSANNE ET AL: "Networks of Molecular Mutations in Acute Myeloid Leukemia and Their Correlations to Cytogenetics and Morphology." XP002272705 Database accession no. PREV200300357666 abstract & BLOOD, vol. 100, no. 11, 16 November 2002 (2002-11-16), page Abstract No. 735, 44th Annual Meeting of the American Society of Hematology; Philadelphia, PA, USA; December 06-10, 2002 ISSN: 0006-4971</p>	1-27
Y	<p>DATABASE BIOSIS 'Online! BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2002 (2002-11-16), NEBEN KAI ET AL: "Acute Myeloid Leukemia with Normal Karyotype and Mutation of the FLT3 or MLL Gene Are Characterized by Specific Gene Expression Profiles." XP002270208 Database accession no. PREV200300336869 abstract & BLOOD, vol. 100, no. 11, 16 November 2002 (2002-11-16), page Abstract No. 2172, 44th Annual Meeting of the American Society of Hematology; Philadelphia, PA, USA; December 06-10, 2002 ISSN: 0006-4971</p>	1-27
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INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP2004/012470

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	<p>& BLOOD, vol. 98, no. 11 Part 1, 16 November 2001 (2001-11-16), pages 717a-718a, 43rd Annual Meeting of the American Society of Hematology, Part 1; Orlando, Florida, USA; December 07-11, 2001 ISSN: 0006-4971</p>	
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INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP2004/012470

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	DUGAS MARTIN ET AL: "Impact of integrating clinical and genetic information." IN SILICO BIOLOGY, vol. 2, no. 3, 2002, pages 383-391, XP001179418 ISSN: 1386-6338 (ISSN print) the whole document	1-27
A	ALIZADEH A ET AL: "THE LYMPHOCHIP: A SPECIALIZED CDNA MICROARRAY FOR THE GENOMIC-SCALE ANALYSIS OF GENE EXPRESSION IN NORMAL AND MALIGNANT LYMPHOCYTES" COLD SPRING HARBOR SYMPOSIA ON QUANTITATIVE BIOLOGY, BIOLOGICAL LABORATORY, COLD SPRING HARBOR, NY, US, vol. 64, no. 1, 1999, pages 71-78, XP001099007 ISSN: 0091-7451 the whole document	1-27
A	DATABASE BIOSIS 'Online! BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2002 (2002-11-16), KOHLMANN ALEXANDER ET AL: "A Simplified and Partially Automated Target Preparation Method for Gene Expression Profiling." XP002269495 Database accession no. PREV200300367771 abstract & BLOOD, vol. 100, no. 11, 16 November 2002 (2002-11-16), page Abstract No. 4287, 44th Annual Meeting of the American Society of Hematology; Philadelphia, PA, USA; December 06-10, 2002 ISSN: 0006-4971	1-27
A	DEUTSCH J M: "Evolutionary algorithms for finding optimal gene sets in microarray prediction." BIOINFORMATICS (OXFORD), vol. 19, no. 1, January 2003 (2003-01), pages 45-52, XP002272405 ISSN: 1367-4803 the whole document	1-27
A	EP 1 109 020 A (CHUGAI PHARMACEUTICAL CO LTD) 20 June 2001 (2001-06-20) the whole document	1-27

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP2004/012470

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>KIYOI HITOSHI ET AL: "FLT3 in human hematologic malignancies." LEUKEMIA & LYMPHOMA. ENGLAND AUG 2002, vol. 43, no. 8, August 2002 (2002-08), pages 1541-1547, XP009027222 ISSN: 1042-8194 the whole document</p> <p style="text-align: center;">-----</p>	1-27

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP2004/012470

Box II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Article 52 (2)(d) EPC - Presentation of information

The claims were only searched with regards to the underlying method of generating a reference data base for distinguishing AML-specific FLT3 length
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-27 (partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-27 (partially)

A method for distinguishing AML_D835 from all other subtypes, the method comprising determining the expression level of the marker DKFZp761H0421. Use of said marker for the manufacture of a diagnostic. A diagnostic kit containing said marker and an apparatus comprising a reference data bank, wherein the reference data bank is obtainable by determining the expression level of DKFZp761H0421.

2. claims: 1-27 (all partially)

Inventions 2-1800

Methods for distinguishing AML-specific FLT3 length mutations from TKD mutations in a sample and methods for distinguishing specific subtypes against all other subtypes and against each other, the method comprising determining individually the expression level of the markers listed in tables 1.1, positions 2-50, tables 1.2-1.8 and in table 2. Use of said markers for the manufacture of diagnostics. Diagnostic kits containing said markers and apparatus comprising a reference data bank, wherein the reference data bank is obtainable by determining the expression levels of said markers.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box II.1

Article 52 (2)(d) EPC - Presentation of information

The claims were only searched with regards to the underlying method of generating a reference data base for distinguishing AML-specific FLT3 length mutations from TDK mutations in a sample.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/EP2004/012470

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 03039443	A	15-05-2003	EP 1308522 A1	07-05-2003
			WO 03039443 A2	15-05-2003
			EP 1470247 A2	27-10-2004
EP 1043676	A	11-10-2000	CA 2304876 A1	09-10-2000
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			WO 0011470 A1	02-03-2000

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